(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
1 April 2004 (01.04.2004)

PCT

(10) International Publication Number
WO 2004/026888 A2

(51) International Patent Classification[7]: C07H

(21) International Application Number: PCT/US2003/029577

(22) International Filing Date: 19 September 2003 (19.09.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/412,479 19 September 2002 (19.09.2002) US

(71) Applicants *(for all designated States except US)*: **COLEY PHARMACEUTICAL GMBH** [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). **UNIVERSITY OF SASKATCHEWAN** [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). **QIAGEN GMBH** [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).

(72) Inventors; and

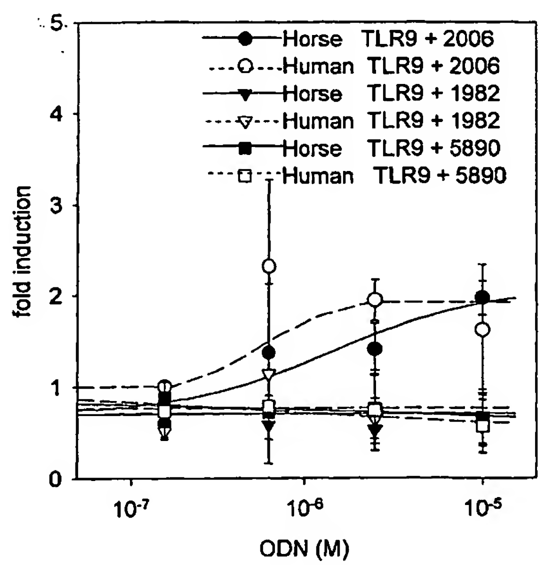
(75) Inventors/Applicants *(for US only)*: **LIPFORD, Grayson, B.** [US/US]; 38 Bates Road, Watertown, MA 02472 (US). **MOOKHERJEE, Neeloffer** [IN/CA]; Apt 408, 2233 Allison Road,, Vancouver, BC V6T IT7 (CA). **BABIUK, Lorne** [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). **BROWNLIE, Robert** [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). **GRIEBEL, Philip** [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). **MUTWIRI, George** [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). **HECKER, Rolf** [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).

(74) Agent: **STEELE, Alan, W.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).

(81) Designated States *(national)*: AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) **Abstract:** Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.

WO 2004/026888 A2

MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) **Designated States** *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001) *Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for biological activity and it is reported that optimal CpG DNA sequences can vary among species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN. Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9 recognizes CpG DNA is not understood.

Summary of the Invention

Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal in response to CpG DNA. To date, the amino acid sequences only of human and murine TLR9 have been reported, and, interestingly, these two species are known to prefer different CpG motifs. The structural basis for this species-specific CpG motif preference has not yet been fully elucidated. The instant invention provides, in part, novel amino acid and nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are useful for elucidating certain key structural features of TLR9. Specifically, comparison of sequences of murine, human, and these novel TLR9 sequences permits identification of areas of highly conserved sequence, areas of group conservation, and areas of hypervariability. In addition, such comparisons permit an assessment of evolutionary relatedness among TLR9 molecules of the various species, as well as an assessment of inter-species homologies. Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9 that may be involved in the CpG binding site, as well as amino acids involved in conferring species specificity for particular CpG motifs. Such information may be used to design and construct novel TLR9 molecules which incorporate specific point or regional mutations and which possess desired ligand binding characteristics. Such information may also be useful in designing and identifying novel ligands for TLR9 of a given species.

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand, such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

TCCATGACGTTTTTGATGTT (SEQ ID NO:39),
TCCATAACGTTTTTGATGTT (SEQ ID NO:40),
TCCATCACGTTTTTGATGTT (SEQ ID NO:41),
TCCATTACGTTTTTGATGTT (SEQ ID NO:42),
TCCATGGCGTTTTTGATGTT (SEQ ID NO:43),
TCCATGCCGTTTTTGATGTT (SEQ ID NO:44),
TCCATGTCGTTTTTGATGTT (SEQ ID NO:45),
TCCATGATGTTTTTGATGTT (SEQ ID NO:46),
TCCATGAAGTTTTTGATGTT (SEQ ID NO:47),
TCCATGAGGTTTTTGATGTT (SEQ ID NO:48),
TCCATGACATTTTTGATGTT (SEQ ID NO:49),
TCCATGACCTTTTTGATGTT (SEQ ID NO:50),
TCCATGACTTTTTTGATGTT (SEQ ID NO:51),
TCCATGACGCTTTTGATGTT (SEQ ID NO:52),
TCCATGACGATTTTGATGTT (SEQ ID NO:53),
TCCATGACGGTTTTGATGTT (SEQ ID NO:54),

TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one embodiment the reporter gene is operatively linked to a promoter sensitive to NF-κB. In one embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test compounds. In one embodiment the response mediated by the TLR9 signal transduction pathway is measured quantitatively and the response mediated by the TLR9 signal transduction pathway associated with each of the plurality of test compounds is compared with a response arising as a result of an interaction between the functional TLR9 and a reference immunostimulatory compound.

Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and human TLR9 sequences alone.

Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine, porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key features of the primary sequences of these and related TLR molecules, including previously

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands. Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI
HHLHNLDFVHLPNVRQLNLKWNCPPPGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
SHTNILVLDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYL
LLSYNLIVKLGAEDLANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSSLHSLN
SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHLASSFKSLVSLQELNMNGIF
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVPW
PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFSMQGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
VEYLDFSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSQNKLHILRPQNLNYLPKSLTKLSFRDNHLSFFNWSSLA
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL
AVAVGTVLPLLQHLCGWDVWYCFHLCLAWLPLLTRGRRSAQALPYDAFVVFDKAQSAVADWVYNELRVRLEERRG
RRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRLLEDRKDVVVLVILRPDA
HRSRYVRLRQRLCRQSVLFWPHQPNGQGSFWAQLSTALTRDNHHFYNRNFCRGPTAE

SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI
HHLHNLDFVHLPNVRQLNLKWNCPPPGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
SHTNILVLDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYL
LLSYNLIVKLGAEDLANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSSLHSLN
SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHLASSFKSLVSLQELNMNGIF
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVPW
PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFSMQGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
VEYLDFSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSQNKLHILRPQNLNYLPKSLTKLSFRDNHLSFFNWSSLA
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG

SEQ ID NO:3 (Rat TLR9)

atggttctctgtcgcaggaccctgcaccccttgtctctcctggtacaggccgcagtgctggctgaggctctggcc
ctgggtaccctgcctgccttcctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttcctg
aagtctgtgcctcacttctctgccgcagaaccccgttccaacatcaccagcctttccttgatcgccaaccgcatc
caccacctgcacaacctcgactttgtccacctgcccaacgtgcgacagctgaacctcaagtggaactgtccgccc
cctggcctcagccccttgcacttctcctgccgcatgaccattgagcccaaaaccttcctggctatgcgcatgctg
gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgcccagctccctgacgaatctgagccta
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac
gggaactgctactacaagaaccccctgcaacggggcggtgaacgtgaccccggacgccttcctgggcttgagcaac
ctcacccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtacctc
ctgctgtcctataacctcatcgtcaagctgggggccgaagacctagccaacctgacctcccttcgaatgcttgat
gtgggtgggaattgccgtcgctgtgatcacgcccccgacctctgtacagaatgccggcagaagtcccttgatctg
caccctcagactttccatcacctgagccaccttgaaggcctggtgctgaaggacagttctctccactcgctgaac
tccaagtggttccagggtctggcgaacctctcggtgctggacctaagcgagaactttctctacgagagcatcaac
aaaaccagcgcctttcagaacctgacccgtctgcgcaagctcgacctgtccttcaattactgcaagaaggtatcg
ttcgcccgcctccacctggcaagttccttcaagagcctggtgtcgctgcaggagctgaacatgaacggcatcttc
ttccgcttactcaacaagaacacgctcaggtggctggctggtctgcccaagctccacacgctgcaccttcaaatg
aatttcatcaaccaggcgcagctcagcgtctttagtaccttccgagcccttcgctttgtggacctgtccaataat
cgcatcagcgggcctccaacgctgtccagagtcgcccccgaaaaggcagacgaggcggagaaggggttccatgg
cctgcaagtctcaccccagctctcccgagcactcccgtctcaaagaacttcatggtcaggtgtaagaacctcaga
ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctcccatctccag
tgtctgagcctgagccacaactgcatcgcgcaggctgtcaatggctctcagttcctgccgctgaccaacctgaag
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctcccacagttgcaggcc

ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg
tccaggttacagaaccttagcctggcacacaatgacattcacagccgcgtgtcctcacgcctctacagcacctca
gtggagtatctggacttcagcggcaacggtgtgggccgcatgtgggacgaggaggacctttacctctatttcttc
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac
tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagtctggcc
ttcctgcccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctaat
ggcacgctcctccagaaactggatgtcagtagcaacagtatcgtctttgtggtcccagccttctttgctctggcg
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctggtttgggcccattgtg
atgaacctgacggttctagacgtgagcagcaaccctctgcattgtgcctgcggtgcaccctttgtagacttactg
ctggaagtgcagaccaaggtgcctggcctggctaacggtgtgaagtgtggcagtccccgccagctgcagggccgc
agcatctttgcgcaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggcctttcactcctg
gctgtggccgtgggcacggtgttgcctttactgcagcatctctgcggctgggacgtctggtactgtttccatctg
tgcctggcatggctacctttgctgacccgtggccggcgcagcgcccaagctctcccttatgatgccttcgtggtg
ttcgataaggcgcagagcgcggttgctgactgggtgtataacgagcttcgagtgcggctagaggagcggcgcggt
cgccgagccctacgcttgtgtctggaggaccgagattggctgcctggccagacactcttcgagaacctctgggcc
tccatctatggcagccgcaagactctgtttgtgctggcccacacggacaaggtcagtggcctcctgcgcaccagc
ttcctgctggctcagcagcgcctgctggaggaccgcaaggacgtggtggtgttggtgatcctgcgccctgatgcc
caccgctcccgctacgtgcgactgcgccagcgcctctgccgccagagtgtgctcttctggccccatcagcccaac
gggcagggcagcttctgggcccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc
tgccggggacctacagcagaatag

SEQ ID NO:4 (Rat TLR9)

atggttctctgtcgcaggaccctgcaccccttgtctctcctggtacaggccgcagtgctggctgaggctctggcc
ctgggtaccctgcctgccttcctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttcctg
aagtctgtgcctcacttctctgccgcagaaccccgttccaacatcaccagcctttccttgatcgccaaccgcatc
caccacctgcacaacctcgactttgtccacctgcccaacgtgcgacagctgaacctcaagtggaactgtccgccc
cctggcctcagccccttgcacttctcctgccgcatgaccattgagcccaaaaccttcctggctatgcgcatgctg
gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgcccagctccctgacgaatctgagccta
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac
gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccggacgccttcctgggcttgagcaac
ctcacccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgcccccagcctggagtacctc
ctgctgtcctataacctcatcgtcaagctggggggccgaagacctagccaacctgacctcccttcgaatgcttgat
gtgggtgggaattgccgtcgctgtgatcacgcccccgacctctgtacagaatgccggcagaagtcccttgatctg
caccctcagactttccatcacctgagccaccttgaaggcctggtgctgaaggacagttctctccactcgctgaac
tccaagtggttccagggtctggcgaacctctcggtgctggacctaagcgagaactttctctacgagagcatcaac
aaaaccagcgcctttcagaacctgacccgtctgcgcaagctcgacctgtccttcaattactgcaagaaggtatcg
ttcgcccgcctccacctggcaagttccttcaagagcctggtgtcgctgcaggagctgaacatgaacggcatcttc
ttccgcttactcaacaagaacacgctcaggtggctggctggtctgcccaagctccacacgctgcaccttcaaatg
aatttcatcaaccaggcgcagctcagcgtctttagtaccttccgagcccttcgctttgtggacctgtccaataat
cgcatcagcgggcctccaacgctgtccagagtcgcccccgaaaggcagacgaggcggagaaggggttccatgg
cctgcaagtctcaccccagctctcccgagcactcccgtctcaaagaacttcatggtcaggtgtaagaacctcaga
ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctcccatctccag
tgtctgagcctgagccacaactgcatcgcgcaggctgtcaatggctctcagttcctgccgctgaccaacctgaag
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctcccacagttgcaggcc
ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg
tccaggttacagaaccttagcctggcacacaatgacattcacagccgcgtgtcctcacgcctctacagcacctca
gtggagtatctggacttcagcggcaacggtgtgggccgcatgtgggacgaggaggacctttacctctatttcttc
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac
tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagtctggcc
ttcctgcccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctaat
ggcacgctcctccagaaactggatgtcagtagcaacagtatcgtctttgtggtcccagccttctttgctctggcg
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctggtttgggcccattgtg
atgaacctgacggttctagacgtgagcagcaaccctctgcattgtgcctgcggtgcaccctttgtagacttactg
ctggaagtgcagaccaaggtgcctggcctggctaacggtgtgaagtgtggcagtccccgccagctgcagggccgc
agcatctttgcgcaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggc

SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRTLNLKWNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS
RTNILVLDPTHLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLL
LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSSLYNLDT
RWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRSLNLSFNYHKKVSFAHLHLAPSFGHLRSLKELDMHGIFF
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR
NLAPRPLDTLRSEDFMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL
DLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC
ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHLHTLLPRALDNLPKSLKHLHLRDNNLAFFNWSSLTLL
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
LKVLDVSANPLHCACGATFVGFLLEVQAAVPGLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLSWNCFGISLLAM
ALGLVVPMLHHLCGWDLWYCFHLCLAWLPHRGQRRGADALFYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRA
LRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILRPDAYRS
RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHHFYNRNFCRGPTTAE

SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRTLNLKWNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS
RTNILVLDPTHLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLL
LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSSLYNLDT
RWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRSLNLSFNYHKKVSFAHLHLAPSFGHLRSLKELDMHGIFF
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR
NLAPRPLDTLRSEDFMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL
DLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC
ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHLHTLLPRALDNLPKSLKHLHLRDNNLAFFNWSSLTLL
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
LKVLDVSANPLHCACGATFVGFLLEVQAAVPGLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLSWNCFG

SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcactgtagctgctgcccggtctgccagccagaccctttggagaagaccccactccctgt
catgggcccccgctgcaccctgcacccccttctctcctggtgcaggtgacagcgctggctgcggctctggccca
gggcaggctgcctgccttcctgccctgtgagctccagccccacggcctggtgaactgcaactggctcttcctgaa
gtccgtgccccacttctcggcggcagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatcca
ccacctgcacgactccgacttcgtccacctgtccagcctacgaactctcaacctcaagtggaactgcccgccggc
tggcctcagccccatgcacttcccctgccacatgaccatcgagcccaacaccttcctggccgtgcccaccctgga
ggagctgaacctgagctacaacagcatcacgaccgtgcctgccctgcccgactccctcgtgtccctgtcgctgag
ccgcaccaacatcctggtgctagaccccacccacctcactggcctacatgccctgcgctacctgtacatggatgg
caactgctactacaagaacccctgccaggggcgctggaggtggtgccgggtgccctcctcggcctgggcaacct
cacacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgcccccagcctggagaccctgct
gttgtcctacaaccacattgtcaccctgacgcctgaggacctggccaatctgactgccctgcgcgtgcttgatgt
gggggggaactgccgccgctgtgaccatgcccgcaacccctgcagggagtgcccaaaggaccaccccaagctgca
ctctgacaccttcagccacctgagccgcctcgaaggcctggtgttgaaagacagttctctctacaacctggacac
caggtggttccgaggcctggacaggctccaagtgctggacctgagtgagaacttcctctacgactgcatcaccaa
gaccacggccttccagggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt
tgcccacctgcacctggcaccctcctttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt
ccgctcgctcagtgagaccacgctccaacctctggtccaactgcctatgctccagaccctgcgcctgcagatgaa
cttcattaaccaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggacaaccg
catcagcggagctgcaaggccagtggccattactagggaggtggatggtagggagagggtctggctgccttccag
gaacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcac
cttggacctgtctcggaacaacctggtgacaatccagtcggagatgtttgctcgcctctcacgcctcgagtgcct
gcgcctgagccacaacagcatctcccaggcggtcaatggctctcagtttgtgccgctgaccagcctgcgggtgct
ggacctgtcccacaacaagctggacctgtatcacgggcgctcgttcacggagctgccgcgcctggaagcactgga
cctcagctacaatagccagccctttaccatgcagggtgtgggccacaacctcagcttcgtggcccagctgcccgc

cctgcgctacctcagcctggcgcacaatgacatccatagccgagtgtcccagcagctctgtagcgcctcactgtg
cgccctggactttagcggcaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaagg
cctaagaagcctagtctggctggacctgtcccagaaccacctgcacaccctcctgccacgtgccctggacaacct
ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgaccctcct
gcccaagctggaaaccctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac
ccagctgcggaggctggacctcagtggcaacagcatcggctttgtgaaccctggcttctttgccctggccaagca
gttagaagagctcaacctcagcgccaatgccctcaagacagtggagccctcctggtttggctcgatggtgggcaa
cctgaaagtcctagacgtgagcgccaaccctctgcactgtgcctgtggggcgaccttcgtgggcttcctgctgga
ggtacaggctgccgtgcctgggctgcccagccgcgtcaagtgtggcagtccggggcagctccagggccatagcat
ctttgcgcaagacctgcgcctctgcctggatgagaccctctcgtggaactgttttggcatctcgctgctggccat
ggccctgggcctggttgtgcccatgctgcaccacctctgcggctgggacctctggtactgcttccacctgtgcct
ggcctggctgccccaccgagggcagcggcggggcgcagacgccctgttctatgatgccttcgtggtctttgacaa
agctcagagtgctgtggccgactgggtgtacaacgagctgcgggtgcagctggaggagcgccgtgggcgccgcgc
actgcgcctgtgcctggaggagcgagactggttacctggcaagacgctcttcgagaacctgtgggcctcagtcta
cagcagccgcaagaccctgtttgtgctggcccacacggaccgtgtcagcggcctcttgcgtgccagtttcctgct
ggcccagcagcgcctgctggaggaccgcaaggacgttgtagtgctggtgatcctgcgccccgatgcctaccgctc
ccgctacgtgcggctgcgccagcgcctctgccgccagagtgtcctcctctggccccaccagccccgtgggcaggg
cagcttctgggcccagctgggcacagccctgaccagggacaaccaccacttctataaccggaacttctgccgggg
ccccacgacagccgaatagcactgagtgacagcccagttgccccagccccccctggatttgcctctctgcctgggg
tgccccaacctgctttgctcagccacaccactgctctgctccctgttccccaccccacccccccagcctggcatgt
aacatgtgcccaataaatgctaccggagggccaagaaaaaaaaaaaaaaaa

SEQ ID NO:8 (Porcine TLR9)

atgggcccccgctgcaccctgcacccccctttctctcctggtgcaggtgacagcgctggctgcggctctggcccag
ggcaggctgcctgccttcctgccctgtgagctccagccccacggcctggtgaactgcaactggctcttcctgaag
tccgtgccccacttctcggcggcagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatccac
cacctgcacgactccgacttcgtccacctgtccagcctacgaactctcaacctcaagtggaactgcccgccggct
ggcctcagccccatgcacttcccctgccacatgaccatcgagcccaacaccttcctggccgtgcccaccctggag
gagctgaacctgagctacaacagcatcacgaccgtgcctgccctgcccgactccctcgtgtccctgtcgctgagc
cgcaccaacatcctggtgctagaccccacccacctcactggcctacatgccctgcgctacctgtacatggatggc
aactgctactacaagaacccctgccagggggcgctggaggtggtgccgggtgccctcctcggcctgggcaacctc
acacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgcccccagcctggagaccctgctg
ttgtcctacaaccacattgtcaccctgacgcctgaggacctggccaatctgactgccctgcgcgtgcttgatgtg
ggggggaactgccgccgctgtgaccatgcccgcaacccctgcagggagtgcccaaaggaccaccccaagctgcac
tctgacaccttcagccacctgagccgcctcgaaggcctggtgttgaaagacagttctctctacaacctggacacc
aggtggttccgaggcctggacaggctccaagtgctggacctgagtgagaacttcctctacgactgcatcaccaag
accacggccttccagggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtccttt
gcccacctgcacctggcaccctcctttgggcacctccggtccctgaaggagctggacatgcatggcatcttcttc
cgctcgctcagtgagaccacgctccaacctctggtccaactgcctatgctccagaccctgcgcctgcagatgaac
ttcattaaccaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggacaaccgc
atcagcggagctgcaaggccagtggccattactagggaggtggatggtagggagagggtctggctgccttccagg
aacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcacc
ttggacctgtctcggaacaacctggtgacaatccagtcggagatgtttgctcgcctctcacgcctcgagtgcctg
cgcctgagccacaacagcatctcccaggcggtcaatggctctcagtttgtgccgctgaccagcctgcgggtgctg
gacctgtcccacaacaagctggacctgtatcacgggcgctcgttcacggagctgccgcgcctggaagcactggac
ctcagctacaatagccagccctttaccatgcagggtgtgggccacaacctcagcttcgtggcccagctgcccgcc
ctgcgctacctcagcctggcgcacaatgacatccatagccgagtgtcccagcagctctgtagcgcctcactgtgc
gccctggactttagcggcaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaaggc
ctaagaagcctagtctggctggacctgtcccagaaccacctgcacaccctcctgccacgtgccctggacaacctc
cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgaccctcctg
cccaagctggaaaccctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc
cagctgcggaggctggacctcagtggcaacagcatcggctttgtgaaccctggcttctttgccctggccaagcag
ttagaagagctcaacctcagcgccaatgccctcaagacagtggagccctcctggtttggctcgatggtgggcaac
ctgaaagtcctagacgtgagcgccaaccctctgcactgtgcctgtggggcgaccttcgtgggcttcctgctggag
gtacaggctgccgtgcctgggctgcccagccgcgtcaagtgtggcagtccggggcagctccagggccatagcatc
tttgcgcaagacctgcgcctctgcctggatgagaccctctcgtggaactgttttggc

SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGTLPAFLPCELQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSLS
HTSILVLGPTHFTGLHALRFLYMDGNCYYMNPCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLEK
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIFF
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR
GLAPGPLDAVSSKDFMPSCNLNFTLDLSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
LSHNKLDLYHGRSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL
KILDVSANPLHCACGAAFVDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGLSLLMVA
LGLAVPMLHHLCGWDLWYCFHLCLAHLPRRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRGRRAL
RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILRPAAYRSR
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNRHFYNRNFCRGPTTAE

SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGTLPAFLPCELQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSLS
HTSILVLGPTHFTGLHALRFLYMDGNCYYMNPCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLEK
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIFF
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR
GLAPGPLDAVSSKDFMPSCNLNFTLDLSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
LSHNKLDLYHGRSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL
KILDVSANPLHCACGAAFVDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFG

SEQ ID NO:11 (Bovine TLR9)

gggaagtgggcgccaagcatccttccctgcagctgcctcccaacctgcccgccagaccctctggagaagccgcat
tccctgtcatgggcccctactgtgccccgcacccccttctctcctggtgcaggcggcggcactggcagcggccc
tggccgagggcaccctgcctgccttcctgccctgtgagctccagccccatggtcaggtggactgcaactggctgt
tcctgaagtctgtgccgcacttttcggctggagccccccgggccaatgtcaccagcctctccttaatctccaacc
gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaactgcc
cgccggccggcctcagccccatgcacttcccctgccgtatgaccatcgagcccaacaccttcctggctgtgccca
ccctggaggagctgaacctgagctacaacggcatcacgaccgtgcctgccctgcccagttccctcgtgtccctgt
cgctgagccacaccagcatcctggtgctaggccccacccacttcaccggcctgcacgccctgcgctttctgtaca
tggacggcaactgctactacatgaacccctgcccgcgggccctggaggtggccccaggcgccctcctcggcctgg
gcaacctcacgcacctgtcgctcaagtacaacaacctcacggaggtgccccgccgcctgcccccccagcctggaca
ccctgctgctgtcctacaaccacattgtcaccctggcacccgaggacctggccaacctgactgccctgcgcgtgc
ttgacgtgggtgggaactgccgccgctgcgaccatgcccgcaacccctgcagggagtgcccaaagaacttcccca
agctgcaccctgacaccttcagtcacctgagccgcctcgaaggcctggtgttgaaggacagttctctctacaaac
tagagaaagattggttccgcggcctgggcaggctccaagtgctcgacctgagtgagaacttcctctatgactaca
tcaccaagaccaccatcttcaacgacctgacccagctgcgcagactcaacctgtccttcaattaccacaagaagg
tgtccttcgcccacctgcacctagcgtcctcctttgggagtctggtgtccctggagaagctggacatgcacggca
tcttcttccgctccctcaccaacatcacgctccagtcgctgacccggctgcccaagctccagagtctgcatctgc
agctgaacttcatcaaccaggcccagctcagcatctttggggccttcccgagcctgctcttcgtggacctgtcgg
acaaccgcatcagcggagccgcgacgccagcggccgccctgggggaggtggacagcagggtggaagtctggcgat
tgcccaggggcctcgctccaggcccgctggacgccgtcagctcaaaggacttcatgccaagctgcaacctcaact
tcaccttggacctgtcacggaacaacctggtgacaatccagcaagagatgtttacccgcctctcccgcctccagt
gcctgcgcctgagccacaacagcatctcgcaggcggttaatggctcccagttcgtgccgctgaccagcctgcgag

tgctcgacctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgccgcagctggaggcac
tggacctcagctacaacagccagcccttcagcatgcagggcgtgggccacaacctcagcttcgtggcccagctgc
cctccctgcgctacctcagccttgcgcacaatggcatccacagccgcgtgtcacagaagctcagcagcgcctcgt
tgcgcgccctggacttcagcggcaactccctgagccagatgtgggccgagggagacctctatctctgcttttca
aaggcttgaggaacctggtccagctggacctgtccgagaaccatctgcacaccctcctgcctcgtcacctggaca
acctgcccaagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccg
tcctgccccggctggaagccctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgcctg
gcatccggctccagaagctggacgtgagcagcaacagcatcggcttcgtgatccccggcttcttcgtccgcgcga
ctcggctgatagagcttaacctcagcgccaatgccctgaagacagtggatccctcctggttcggttccttagcag
ggaccctgaaatcctagacgtgagcgccaacccgctccactgcgcctgcggggcggcctttgtggacttcctgc
tggagagacaggaggccgtgcccgggctgtccaggcgcgtcacatgtggcagtccgggccagctccagggccgca
gcatcttcacacaggacctgcgcctctgcctggatgagaccctctccttggactgctttggcctctcactgctaa
tggtggcgctgggcctggcagtgcccatgctgcaccacctctgtggctgggacctctggtactgcttccacctgt
gtctggcccatttgccccgacggcggcggcagcggggcgaggacaccctgctctatgatgccgtcgtggtcttcg
acaaggtgcagagtgcagtggctgattgggtgtacaacgagctccgcgtgcagctggaggagcgccgggggcgcc
gggcgctccgcctctgcctggaggagcgagactggctccctggtaagacgctcttcgagaacctgtgggcctcgg
tctacagcagccgcaagaccatgttcgtgctggaccacacggaccgggtcagcggcctcctgcgcgccagcttcc
tgctggcccagcagcgcctgttggaggaccgcaaggacgtcgtagtgctggtgatcctgcgccccgccgcctatc
ggtcccgctacgtgcggctgcgccagcgcctctgccgccagagcgtcctcctctggccccaccagcccagtggcc
agggtagtttctgggccaacctgggcatagccctgaccagggacaaccgtcacttctataaccggaacttctgcc
ggggccccacgacagccgaatagcacagagtgactgcccag

SEQ ID NO:12 (Bovine TLR9)

atgggcccctactgtgccccgcacccctttctctcctggtgcaggcggcggcactggcagcggccctggccgag
ggcaccctgcctgccttcctgccctgtgagctccagccccatggtcaggtggactgcaactggctgttcctgaag
tctgtgccgcactttcggctggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac
cacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaactgcccgccggcc
ggcctcagccccatgcacttcccctgccgtatgaccatcgagcccaacaccttcctggctgtgcccaccctggag
gagctgaacctgagctacaacggcatcacgaccgtgcctgccctgcccagttccctcgtgtccctgtcgctgagc
cacaccagcatcctggtgctaggccccacccacttcaccggcctgcacgccctgcgctttctgtacatggacggc
aactgctactacatgaacccctgcccgcgggccctggaggtggccccaggcgccctcctcggcctgggcaacctc
acgcacctgtcgctcaagtacaacaacctcacggaggtgccccgccgcctgcccccccagcctggacaccctgctg
ctgtcctacaaccacattgtcaccctggcacccgaggacctggccaacctgactgccctgcgcgtgcttgacgtg
ggtgggaactgccgccgctgcgaccatgcccgcaacccctgcagggagtgcccaaagaacttccccaagctgcac
cctgacaccttcagtcacctgagccgcctcgaaggcctggtgttgaaggacagttctctctacaaactagagaaa
gattggttccgcggcctgggcaggctccaagtgctcgacctgagtgagaacttcctctatgactacatcaccaag
accaccatcttcaacgacctgacccagctgcgcagactcaacctgtccttcaattaccacaagaaggtgtccttc
gcccacctgcacctagcgtcctcctttgggagtctggtgtccctggagaagctggacatgcacggcatcttcttc
cgctccctcaccaacatcacgctccagtcgctgacccggctgcccaagctccagagtctgcatctgcagctgaac
ttcatcaaccaggcccagctcagcatctttggggccttcccgagcctgctcttcgtggacctgtcggacaaccgc
atcagcggagccgcgacgccagcggccgccctgggggaggtggacagcagggtggaagtctggcgattgcccagg
ggcctcgctccaggcccgctggacgccgtcagctcaaaggacttcatgccaagctgcaacctcaacttcaccttg
gacctgtcacggaacaacctggtgacaatccagcaagagatgtttacccgcctctcccgcctccagtgcctgcgc
ctgagccacaacagcatctcgcaggcggttaatggctcccagttcgtgccgctgaccagcctgcgagtgctcgac
ctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgccgcagctggaggcactggacctc
agctacaacagccagcccttcagcatgcagggcgtgggccacaacctcagcttcgtggcccagctgccctccctg
cgctacctcagccttgcgcacaatggcatccacagccgcgtgtcacagaagctcagcagcgcctcgttgcgcgcc
ctggacttcagcggcaactccctgagccagatgtgggccgagggagacctctatctctgcttttcaaaggcttg
aggaacctggtccagctggacctgtccgagaaccatctgcacaccctcctgcctcgtcacctggacaacctgccc
aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccgtcctgccc
cggctggaagccctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgcctggcatccgg
ctccagaagctggacgtgagcagcaacagcatcggcttcgtgatccccggcttcttcgtccgcgcgactcggctg
atagagcttaacctcagcgccaatgccctgaagacagtggatccctcctggttcggttccttagcagggaccctg
aaatcctagacgtgagcgccaacccgctccactgcgcctgcggggcggcctttgtggacttcctgctggagaga
caggaggccgtgcccgggctgtccaggcgcgtcacatgtggcagtccgggccagctccagggccgcagcatcttc
acacaggacctgcgcctctgcctggatgagaccctctccttggactgctttggc

SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI
HHLHDSDFAQLSNLQKLNLKWNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNLTTVPRSLPPSLEYL
LLSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN
PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGSLLSLQELDMHGIF
FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFSMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL
WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG
SLEVLDVSANPLHCACGAAFVDFLLQVQAAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV
VALGLAMPMLHHLCGWDLWYCFHLGLAWLPRRGWQRGADALSYDAFVVFDKAQSAVADWVYNELRVRLEERRGRR
ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDARR
SRYVRLRQRLCRQSVLFWPHQPSGQRSFWAQLGMALTRDNRHFYNQNFCRGPTMAE

SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI
HHLHDSDFAQLSNLQKLNLKWNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNLTTVPRSLPPSLEYL
LLSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN
PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGSLLSLQELDMHGIF
FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFSMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL
WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG
SLEVLDVSANPLHCACGAAFVDFLLQVQAAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG

SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgcgtgaagggactgcgagcacaaagcatcctcctctgcagctgctgcccagtg
tgccagctggaccctctggatcatctcccactccctgtcatgggcccttgccatggtgccctgcagcccctgtct
ctcctggtgcaggcggccatgctggccgtggctctggcccaaggcaccctgcctcccttcctgccctgtgagctc
cagccccacggcctggtgaactgcaactggctgttcctgaagtccgtgccccacttctcagcagcagcaccccgg
gacaatgtcaccagcctttccttgctctccaaccgcatccaccacctccacgactccgactttgcccaactgtcc
aacctgcagaaactcaacctcaaatggaactgcccgccagccggcctcagccccatgcacttcccctgccacatg
accatcgagcccaacactttcctggctgtacccaccctggaggagctgaacctgagctacaacggcatcacgact
gtgcctgccctgcccagctccctcgtgtccctgatcctgagccgcaccaacatcctgcagctagaccccaccagc
ctcacgggcctgcatgccctgcgcttcctatacatggatggcaactgctactacaagaacccctgcgggcgggcc
ctggaggtggccccaggcgccctccttggcctgggcaacctcacccacctgtcactcaagtacaacaacctcaca
acggtgccccgcagcctgcccccctagcctggagtacctgctgttgtcctacaaccacattgtcaccctggcacct
gaggacctggccaatctgactgccctgcgtgtgctcgatgtgggtggaaactgccgccgctgtgaccatgcacgc
aacccctgcgtggagtgcccacataaattcccccagctgcactccgacaccttcagccacctaagccgcctagaa
ggcctcgtgttgaaggatagttctctctaccagctgaaccccagatggttccgtggcctgggcaacctcacagtg
ctcgacctgagtgagaacttcctctacgactgcatcaccaaaaccaaggcattccagggcctggcccagctgcga
agactcaacttgtccttcaattaccataagaaggtgtccttcgcccacctgacgctggcaccctccttcgggagc
ctgctctccctgcaggaactggacatgcatggcatcttcttccgctcactcagccagaagacgctccagccactg
gcccgcctgcccatgctccagcgtctgtatctgcagatgaacttcatcaaccaggcccagctcggcatcttcaag
gacttccctggtctgcgctacatagacctgtcagacaaccgcatcagtggagctgtggagccggtggccaccaca
ggggaggtggatggtgggaagaaggtctggctgacatccagggacctcactccaggcccactggacacccccagc
tctgaggacttcatgccaagctgcaagaacctcagcttcaccttggacctgtcacggaacaacctggtaacagtc
cagccagagatgtttgcccagctctcgcgcctccagtgcctgcgcctgagccacaacagcatctcgcaggcggtc

aatggctcacagttcgtgccactgaccagcctgcaggtgctggacctgtcccataacaaactggacctgtaccat
gggcgctcgtttacggagctgccgcgactggaggccctggacctcagctacaacagccagcccttcagcatgcgg
ggtgtgggccacaacctcagctttgtggcccagctgcccaccctgcgctacctcagcctggcacacaatggcatc
cacagccgtgtgtcccagcagctctgcagcacctcgctgtgggccctggacttcagcggcaattccctgagccag
atgtgggctgagggagacctctatctccgcttcttccaaggcctgagaagcctaatccggctagacctgtcccag
aatcgtctgcataccctcctgccatgcaccctgggcaacctccccaagagcttgcagctgctgcgtctccgtaac
aattacctggccttcttcaattggagcagcctgaccctcctgcccaacctggaaaccctggacctggctggaaac
cagctgaaggctctgagcaatggcagcctgccttctggcacccagctccagaggctggacgtcagcaggaacagc
atcatcttcgtggtccctggcttctttgctctggccacgaggctgcgagagctcaacctcagtgccaacgccctc
aggacagaggagccctcctggtttggtttcctagcaggctcccttgaagtcctagatgtgagcgccaaccctctg
cactgcgcctgtggggcagcctttgtggacttcctgctgcaggttcaggctgccgtgcctggtctgcccagccgc
gtcaagtgtggcagtccgggccagctccagggccgcagcatcttcgcacaagacctgcgcctctgcctggacaag
tccctctcctgggactgtttggtctctcattgctggttgtggccctgggcctggccatgcctatgttgcaccac
ctctgcggctgggacctctggtactgcttccacctgggcctggcctggctgccccggcgggggtggcagcggggc
gcggatgccctgagctatgatgcctttgtggtcttcgacaaggcacagagcgcagtggccgactgggtgtacaat
gaactgcgggtgcggctagaggagcgccgtgggcgccgggcgctccgcctgtgtctggaggagcgtgactggcta
cctggcaagacgctgttcgaaaacctgtgggcctcagtctacagcagccgcaagatgctgtttgtgctggcccac
acggaccaggtcagtggcctcttgcgtgccagcttcctgctggcccagcagcgtctgctggaggaccgcaaggac
gttgtggtgctggtaatcctgagccctgacgcccgccgttcccgttacgtgcggctgcgccagcgcctctgccgc
cagagtgtcctcttctggccccaccagcctagtggccagcgcagcttctgggcccagctaggcatggccctgacc
agggacaaccgccacttctataaccagaacttctgccggggcccgacgatggctgagtagcacagagtgacagcc
tggcatgtacaaccccagccctgaccttgcctctctgcctatgatgcccagtctgcctcactctgtgacgcccc
tgctctgcctccgccaccctcaccctggcatacagcaggcactcaataaatgccactggcaggccaaacagcca
aaaaaaaaaaaaaaa

SEQ ID NO:16 (Equine TLR9)

atgggcccttgccatggtgccctgcagcccctgtctctcctggtgcaggcggccatgctggccgtggctctggcc
caaggcaccctgcctcccttcctgccctgtgagctccagccccacggcctggtgaactgcaactggctgttcctg
aagtccgtgccccacttctcagcagcagcaccccgggacaatgtcaccagcctttccttgctctccaaccgcatc
caccacctccacgactccgactttgcccaactgtccaacctgcagaaactcaacctcaaatggaactgcccgcca
gccggcctcagccccatgcacttcccctgccacatgaccatcgagcccaacactttcctggctgtacccaccctg
gaggagctgaacctgagctacaacggcatcacgactgtgcctgccctgcccagctccctcgtgtccctgatcctg
agccgcaccaacatcctgcagctagaccccaccagcctcacgggcctgcatgccctgcgcttcctatacatggat
ggcaactgctactacaagaacccctgcgggcgggccctggaggtggccccaggcgccctccttggcctgggcaac
ctcacccacctgtcactcaagtacaacaacctcacaacggtgccccgcagcctgccccctagcctggagtacctg
ctgttgtcctacaaccacattgtcaccctggcacctgaggacctggccaatctgactgccctgcgtgtgctcgat
gtgggtggaaactgccgccgctgtgaccatgcacgcaacccctgcgtggagtgcccacataaattcccccagctg
cactccgacaccttcagccacctaagccgcctagaaggcctcgtgttgaaggatagttctctctaccagctgaac
cccagatggttccgtggcctgggcaacctcacagtgctcgacctgagtgagaacttcctctacgactgcatcacc
aaaaccaaggcattccagggcctggcccagctgcgaagactcaacttgtccttcaattaccataagaaggtgtcc
ttcgcccacctgacgctggcaccctccttcgggagcctgctctccctgcaggaactggacatgcatggcatcttc
ttccgctcactcagccagaagacgctccagccactggcccgcctgcccatgctccagcgtctgtatctgcagatg
aacttcatcaaccaggcccagctcggcatcttcaaggacttccctggtctgcgctacatagacctgtcagacaac
cgcatcagtggagctgtggagccggtggccaccacaggggaggtggatggtgggaagaaggtctggctgacatcc
agggacctcactccaggcccactggacacccccagctctgaggacttcatgccaagctgcaagaacctcagcttc
accttggacctgtcacggaacaacctggtaacagtccagccagagatgtttgcccagctctcgcgcctccagtgc
ctgcgcctgagccacaacagcatctcgcaggcggtcaatggctcacagttcgtgccactgaccagcctgcaggtg
ctggacctgtcccataacaaactggacctgtaccatgggcgctcgtttacggagctgccgcgactggaggccctg
gacctcagctacaacagccagcccttcagcatgcggggtgtgggccacaacctcagctttgtggcccagctgccc
accctgcgctacctcagcctggcacacaatggcatccacagccgtgtgtcccagcagctctgcagcacctcgctg
tgggccctggacttcagcggcaattccctgagccagatgtgggctgagggagacctctatctccgcttcttccaa
ggcctgagaagcctaatccggctagacctgtcccagaatcgtctgcataccctcctgccatgcaccctgggcaac
ctccccaagagcttgcagctgctgcgtctccgtaacaattacctggccttcttcaattggagcagcctgaccctc
ctgcccaacctggaaaccctggacctggctggaaaccagctgaaggctctgagcaatggcagcctgccttctggc
acccagctccagaggctggacgtcagcaggaacagcatcatcttcgtggtccctggcttctttgctctggccacg
aggctgcgagagctcaacctcagtgccaacgccctcaggacagaggagccctcctggtttggtttcctagcaggc
tcccttgaagtcctagatgtgagcgccaaccctctgcactgcgcctgtggggcagcctttgtggacttcctgctg

caggttcaggctgccgtgcctggtctgcccagccgcgtcaagtgtggcagtccgggccagctccagggccgcagc
atcttcgcacaagacctgcgcctctgcctggacaagtccctctcctgggactgttttggt

SEQ ID NO:17 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAFLPCELQPRGKVNCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSLS
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQAVEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLEK
DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFNYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIFF
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWPR
GLAPGPLAAVSAKDFMPSCNLNFTLDLSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETL
NILDVSANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSLDCFGFSLLMVA
LGLAVPMLHHLCGWDLWYCFHLCLAHLPRRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRAL
RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILRPAAYRSR
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAFLPCELQPRGKVNCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSLS
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQAVEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLEK
DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFNYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIFF
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWPR
GLAPGPLAAVSAKDFMPSCNLNFTLDLSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETL
NILDVSANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSLDCFG

SEQ ID NO:19 (Ovine TLR9)

gtcggcacgggaagtgagcgccaagcatccttccctgcagctgccgcccaacttgcccgccagaccctctggaga
agccgcattccctgccatgggcccctactgtgccccgcaccccctttctctcctggtgcaggcggcggcgctggc
agcagccctggcccagggcaccctgcctgccttcctgccctgtgagctccagccccggggtaaggtgaactgcaa
ctggctgttcctgaagtctgtgccgcgcttttcggccggagcccccgggccaatgtcaccagcctctccttaat
ctccaaccgcatccaccacttgcacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtg
gaactgcccgccggccggcctcagccccatgcacttcccctgccgcatgaccatcgagcccaacaccttcctggc
tgtgcccaccctggaggagctgaacctgagctacaatggcatcacgaccgtgcctgccctgcccagttctctcgt
atccctgtcgctgagccgcaccagcatcctggtgctaggccccacccacttcaccggcctgcacgccctgcgctt
tctgtacatggacggcaactgctactataagaacccctgccagcaggccgtggaggtggccccaggcgccctcct
tggcctgggcaacctcacgcacctgtcgctcaagtacaacaacctcacggaggtgccccgccgcctgcccccccag
cctggacaccctgctgctgtcctacaaccacatcatcaccctggcacccgaggacctggccaatctgactgccct
gcgtgtgcttgatgtgggcgggaactgccgccgctgcgaccacgcccgcaacccctgcagggagtgcccaaagaa
cttccccaagctgcaccctgacaccttcagccacctgagccgcctcgaaggcctggtgttgaaggacagttctct
ctacaaactagagaaagactggttccgcggcctgggcaggctccaagtgctcgacctgagtgagaacttcctcta
tgactacatcaccaagaccaccatcttcaggaacctgacccagctgcgcagactcaacctgtccttcaattacca
caagaaggtgtccttcgcccacctgcaactggcaccctcctttggggggcctggtgtccctggagaagctggacat
gcacggcatcttcttccgctccctcaccaacaccacgctccggccgctgacccagctgcccaagctccagagtct
gagtctgcagctgaacttcatcaaccaggccgagctcagcatctttggggccttcccgagcctgctcttcgtgga
cctgtcggacaaccgcatcagcggagctgcgaggccggtggccgccctcggggaggtggacagcggggtggaagt
ctggcggtggcccaggggcctcgctccaggcccgctggccgccgtcagcgcaaaggacttcatgccaagctgcaa

cctcaacttcaccttggacctgtcacggaacaacctggtgacgatccagcaggagatgtttacccgcctctcccg
cctccagtgcctgcgcctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgccgctgacccg
cctgcgagtgctcgacctgtcctacaacaagctggacctgtaccatggcgctcgttcacggagctgccgcagct
ggaggcactggacctcagctacaacagccagcccttcagcatgcagggcgtgggccacaacctcagcttcgtggc
ccagctgccgtccctgcgctacctcagccttgcgcacaacggcatccacagccgcgtgtcacagaagctcagcag
cgcctcgctgcgcgccctggacttcagcggcaactccctgagccagatgtgggccgagggagacctctatctctg
cttcttcaaaggcttgaggaacctggtccagctggacctgtccaagaaccacctgcacaccctcctgcctcgtca
cctggataacctgcccaagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcag
cctgactgttctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcct
gccacctggcacccggctccagaagctggacgtgagcagcaacagcatcggctttgtgacccctggcttctttgt
ccttgccaaccggctgaaagagcttaacctcagcgccaacgccctgaagacagtggatcccttctggttcggtcg
cttaacagagaccctgaatatcctagacgtgagcgccaacccgctccactgtgcctgcggggcggcctttgtgga
cttcctgctggagatgcaggcggccgtgcctgggctgtccaggcgcgtcacgtgtggcagtccgggccagctcca
gggccgcagcatcttcgcacaggacctgcgcctctgcctggatgagaccctctccttggactgctttggcttctc
gctgctaatggtggcgctgggcctggcggtgcccatgctgcaccacctctgtggctgggacctgtggtactgctt
ccacctgtgtctggcccatttgccccgacggcggcggcagcggggcgaggacaccctgctctacgatgccttcgt
ggtcttcgacaaggcgcagagtgcagtggccgactgggtgtacaacgagctccgcgtgcagctggaggagcgccg
cgggcgccgggcgctccgcctctgcctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg
ggcctcggtctacagcagccgtaagaccatgttcgtgctggaccacacggaccgggtcagtggcctcctgcgcgc
cagcttcctgctggcccagcagcgcctgttggaggaccgcaaggatgtcgtggtgctggtgatcctgcgccccgc
cgcctaccggtcccgctacgtgcggctgcgccagcgcctctgccgccagagcgtcctcctctggccccaccagcc
cagtggccagggtagcttctgggccaacctgggcatggccctgaccagggacaaccgccacttctataaccggaa
cttctgccggggccccacgacagccgaatagcacagagtgactgcccag

SEQ ID NO:20 (Ovine TLR9)

atgggcccctactgtgccccgcacccccctttctctcctggtgcaggcggcggcgctggcagcagccctggcccag
ggcaccctgcctgccttcctgccctgtgagctccagccccggggtaaggtgaactgcaactggctgttcctgaag
tctgtgccgcgcttttcggccggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac
cacttgcacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaactgcccgccggcc
ggcctcagccccatgcacttcccctgccgcatgaccatcgagcccaacaccttcctggctgtgcccaccctggag
gagctgaacctgagctacaatggcatcacgaccgtgcctgccctgcccagttctctcgtatccctgtcgctgagc
cgcaccagcatcctggtgctaggccccacccacttcaccggcctgcacgccctgcgctttctgtacatggacggc
aactgctactataagaacccctgccagcaggccgtggaggtggccccaggcgccctccttggcctgggcaacctc
acgcacctgtcgctcaagtacaacaacctcacggaggtgccccgccgcctgcccccccagcctggacaccctgctg
ctgtcctacaaccacatcatcaccctggcacccgaggacctggccaatctgactgccctgcgtgtgcttgatgtg
ggcgggaactgccgccgctgcgaccacgcccgcaacccctgcagggagtgcccaaagaacttccccaagctgcac
cctgacaccttcagccacctgagccgcctcgaaggcctggtgttgaaggacagttctctctacaaactagagaaa
gactggttccgcggcctgggcaggctccaagtgctcgacctgagtgagaacttcctctatgactacatcaccaag
accaccatcttcaggaacctgacccagctgcgcagactcaacctgtccttcaattaccacaagaaggtgtccttc
gcccacctgcaactggcaccctcctttggggggcctggtgtccctggagaagctggacatgcacggcatcttcttc
cgctccctcaccaacaccacgctccggccgctgacccagctgcccaagctccagagtctgagtctgcagctgaac
ttcatcaaccaggccgagctcagcatctttggggccttcccgagcctgctcttcgtggacctgtcggacaaccgc
atcagcggagctgcgaggccggtggccgccctcggggaggtggacagcggggtggaagtctggcggtggcccagg
ggcctcgctccaggcccgctggccgccgtcagcgcaaaggacttcatgccaagctgcaacctcaacttcaccttg
gacctgtcacggaacaacctggtgacgatccagcaggagatgtttacccgcctctcccgcctccagtgcctgcgc
ctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgccgctgacccgcctgcgagtgctcgac
ctgtcctacaacaagctggacctgtaccatggcgctcgttcacggagctgccgcagctggaggcactggacctc
agctacaacagccagcccttcagcatgcagggcgtgggccacaacctcagcttcgtggcccagctgccgtccctg
cgctacctcagccttgcgcacaacggcatccacagccgcgtgtcacagaagctcagcagcgcctcgctgcgcgcc
ctggacttcagcggcaactccctgagccagatgtgggccgagggagacctctatctctgcttcttcaaaggcttg
aggaacctggtccagctggacctgtccaagaaccacctgcacaccctcctgcctcgtcacctggataacctgccc
aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc
cagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcctgccacctggcacccgg
ctccagaagctggacgtgagcagcaacagcatcggctttgtgacccctggcttctttgtccttgccaaccggctg
aaagagcttaacctcagcgccaacgccctgaagacagtggatcccttctggttcggtcgcttaacagagaccctg
aatatcctagacgtgagcgccaacccgctccactgtgcctgcggggcggcctttgtggacttcctgctggagatg

caggcggccgtgcctgggctgtccaggcgcgtcacgtgtggcagtccgggccagctccagggccgcagcatcttc
gcacaggacctgcgcctctgcctggatgagaccctctccttggactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are publicly availiable. For example, an amino acid sequence for canine TLR9 is available as GenBank accession number BAC65192 and its corresponding nucleotide sequence is available as GenBank accession number AB104899. An amino acid sequence for feline TLR9 is available as GenBank accession number AAN15751 and its corresponding nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of canine TLR9 (See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides 91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID NO:25.

SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPAFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI
HHLHDYDFVHFVHLRRLNLKWNCPPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLSYNSITTVPALPSSLVSLSL
SRTNILVLDPATLAGLYALRFLFLDGNCYYKNPCQQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL

LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFPQLHPNTFGHLSHLEGLVLRDSSLYSLD
PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSFGSLLSLQELDIHGIF
FRSLSKTTLQSLAHLPMLQRLHLQLNFISQAQLSIFGAFPGLRYVDLSDNRISGAAEPAAATGEVEADCGERVWP
QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFSMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA
SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFSLSL
LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRRGVDALAYDAFVVFDKAQSSVADWVYNELRVQLEERRG
RRALRLCLEERDWVPGKTLFENLWASVYSSRKTLFVLARTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILCPDA
HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNRHFYNQNFCRGPTTA

SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPAFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI
HHLHDYDFVHFVHLRRLNLKWNCPPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLSYNSITTVPALPSSLVSLSL
SRTNILVLDPATLAGLYALRFLFLDGNCYYKNPCQQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL
LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFPQLHPNTFGHLSHLEGLVLRDSSLYSLD
PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSFGSLLSLQELDIHGIF
FRSLSKTTLQSLAHLPMLQRLHLQLNFISQAQLSIFGAFPGLRYVDLSDNRISGAAEPAAATGEVEADCGERVWP
QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFSMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA
SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFS

SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttcctgcagctgctgcccagcctgccagccagaccctctggagaag
cccccgctccctgtcatgggcccctgccgtggcgccctgcacccccctgtctctcctggtgcaggctgccgcgcta
gccctggccctggcccagggcaccctgcctgccttcctgccctgtgagctccagccccatggcctggtgaactgc
aactggctgttcctcaagtccgtgccccgcttctcggcagctgcaccccgcggtaacgtcaccagcctttccttg
tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccacctgcggcgtctcaatctcaag
tggaactgcccgcccgccagcctcagccccatgcactttccctgtcacatgaccattgagcccaacaccttcctg
gctgtgcccaccctagaggacctgaatctgagctataacagcatcacgactgtgcccgccctgcccagttcgctt
gtgtccctgtccctgagccgcaccaacatcctggtgctggaccctgccaccctggcaggcctttatgccctgcgc
ttcctgttcctggatggcaactgctactacaagaacccctgccagcaggccctgcaggtggccccaggtgccctc
ctgggcctgggcaacctcacacacctgtcactcaagtacaacaacctcaccgtggtgccgcggggcctgcccccc
agcctggagtacctgctcttgtcctacaaccacatcatcaccctggcacctgaggacctggccaatctgactgcc
ctgcgtgtcctcgatgtgggtgggaactgtcgccgctgtgaccatgcccgtaacccctgcagggagtgccccaag
ggcttcccccagctgcaccccaacaccttcggccacctgagccacctcgaaggcctggtgttgagggacagctct
ctctacagcctggaccccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttcctg
tatgactgcatcaccaaaaccaaagccttctacggcctggcccggctgcgcagactcaacctgtccttcaattat
cataagaaggtgtcctttgcccacctgcatctggcatcctccttcgggagcctactgtccctgcaggagctggac
atacatggcatcttcttccgctcgctcagcaagaccacgctccagtcgctggcccacctgcccatgctccagcgt
ctgcatctgcagttgaactttatcagccaggcccagctcagcatcttcggcgccttccctggactgcggtacgtg
gacttgtcagacaaccgcatcagtggagctgcagagcccgcggctgccacaggggaggtagaggcagactgtggg
gagagagtctggccacagtcccgggaccttgctctgggcccactgggcaccccggctcagaggccttcatgccg
agctgcaggaccctcaacttcaccttggacctgtctcggaacaacctagtgactgttcagccggagatgtttgtc
cggctggcgcgcctccagtgcctgggcctgagccacaacagcatctcgcaggcggtcaatggctcgcagttcgtg
cctctgagcaacctgcgggtgctggacctgtcccataacaagctggacctgtaccacgggcgctcgttcacggag
ctgccgcggctggaggccttggacctcagctacaacagccagcccttcagcatgcggggcgtgggccacaatctc
agctttgtggcacagctgccagccctgcgctacctcagcctggcgcacaatggcatccacagccgcgtgtcccag
cagctccgcagcgcctcgctccgggccctggacttcagtggcaataccctgagccagatgtgggccgagggagac
ctctatctccgcttcttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgcctgcataccctc
ctgccacgcaacctggacaacctccccaagagcctgcggctcctgcggctccgtgacaattacctggctttcttc
aactggagcagcctggccctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagc

aatggcagcttgcccaacggcacccagctccagaggctggacctcagcggcaacagcatcggcttcgtggtcccc
agctttttgccctggccgtgaggcttcgagagctcaacctcagcgccaacgccctcaagacggtggagccctcc
tggtttggttccctggcgggtgccctgaaagtcctagacgtgaccgccaaccccttgcattgcgcttgcggcgca
accttcgtggacttcttgctggaggtgcaggctgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccg
ggccagctccagggccgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgt
ttcagcctctcgctgctggctgtggccctgagcctggctgtgcccatgctgcaccagctctgtggctgggacctc
tggtactgcttccacctgtgcctggcctggctgccccggcgggggcggcggcggggtgtggatgccctggcctat
gacgccttcgtggtcttcgacaaggcgcagagctcggtggcggactgggtgtacaatgagctgcgggtacagcta
gaggagcgccgtgggcgccgggcgctacgcctgtgtctggaggaacgtgactgggtacccggcaaaaccctcttc
gagaacctctgggcctcagtttacagcagccgcaagacgctgtttgtgctggcccgcacggacagagtcagcggc
ctcctgcgtgccagcttcctgctggcccaacagcgcctgctggaggaccgcaaggacgtcgtggtgctggtgatc
ctgtgccccgacgcccaccgctcccgctatgtgcggctgcgccagcgcctctgccgccagagtgtcctcctctgg
ccccaccagcccagtggccagcgcagcttctgggcccagctgggcacggccctgaccagggacaaccgccacttc
tacaaccagaacttctgccggggccccacgacagcctgataggcagacagcccagcaccttcgcgcccctacacc
ctgcctgtctgtctgggatgcccgacctgctggctctacaccgccgctctgtctcccctacacccagccctggca
taaagcgaccgctcaataaatgctgctggtagac

SEQ ID NO:24 (Canine TLR9)

atgggcccctgccgtggcgccctgcacccccctgtctctcctggtgcaggctgccgcgctagccctggccctggcc
cagggcaccctgcctgccttcctgccctgtgagctccagccccatggcctggtgaactgcaactggctgttcctc
aagtccgtgccccgcttctcggcagctgcaccccgcggtaacgtcaccagcctttccttgtactccaaccgcatc
caccacctccatgactatgactttgtccacttcgtccacctgcggcgtctcaatctcaagtggaactgcccgccc
gccagcctcagccccatgcactttccctgtcacatgaccattgagcccaacaccttcctggctgtgcccacccta
gaggacctgaatctgagctataacagcatcacgactgtgcccgccctgcccagttcgcttgtgtccctgtccctg
agccgcaccaacatcctggtgctggaccctgccaccctggcaggcctttatgccctgcgcttcctgttcctggat
ggcaactgctactacaagaaccccctgccagcaggccctgcaggtggccccaggtgccctcctgggcctgggcaac
ctcacacacctgtcactcaagtacaacaacctcaccgtggtgccgcggggcctgccccccagcctggagtacctg
ctcttgtcctacaaccacatcatcaccctggcacctgaggacctggccaatctgactgccctgcgtgtcctcgat
gtgggtgggaactgtcgccgctgtgaccatgcccgtaacccctgcagggagtgccccaagggcttcccccagctg
caccccaacaccttcggccacctgagccacctcgaaggcctggtgttgagggacagctctctctacagcctggac
cccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttcctgtatgactgcatcacc
aaaaccaaagccttctacggcctggcccggctgcgcagactcaacctgtccttcaattatcataagaaggtgtcc
tttgcccacctgcatctggcatcctccttcgggagcctactgtccctgcaggagctggacatacatggcatcttc
ttccgctcgctcagcaagaccacgctccagtcgctggcccacctgcccatgctccagcgtctgcatctgcagttg
aactttatcagccaggcccagctcagcatcttcggcgccttccctggactgcggtacgtggacttgtcagacaac
cgcatcagtggagctgcagagcccgcggctgccacaggggaggtagaggcagactgtggggagagagtctggcca
cagtcccgggaccttgctctgggcccactgggcaccccggctcagaggccttcatgccgagctgcaggaccctc
aacttcaccttggacctgtctcggaacaacctagtgactgttcagccggagatgtttgtccggctggcgcgcctc
cagtgcctgggcctgagccacaacagcatctcgcaggcggtcaatggctcgcagttcgtgcctctgagcaacctg
cgggtgctggacctgtcccataacaagctggacctgtaccacgggcgctcgttcacggagctgccgcggctggag
gccttggacctcagctacaacagccagcccttcagcatgcggggcgtgggccacaatctcagctttgtggcacag
ctgccagccctgcgctacctcagcctggcgcacaatggcatccacagccgcgtgtcccagcagctccgcagcgcc
tcgctccgggccctggacttcagtggcaataccctgagccagatgtgggccgagggagacctctatctccgcttc
ttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgcctgcataccctcctgccacgcaacctg
gacaacctccccaagagcctgcggctcctgcggctccgtgacaattacctggctttcttcaactggagcagcctg
gccctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc
aacggcacccagctccagaggctggacctcagcggcaacagcatcggcttcgtggtccccagctttttgccctg
gccgtgaggcttcgagagctcaacctcagcgccaacgccctcaagacggtggagccctcctggtttggttccctg
gcgggtgccctgaaagtcctagacgtgaccgccaaccccttgcattgcgcttgcggcgcaaccttcgtggacttc
ttgctggaggtgcaggctgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccgggccagctccagggc
cgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgtttcagc

SEQ ID NO:25 (Feline TLR9)

MGPCHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI
HHLHDSDFVHLSSLRRLNLKWNCPPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLVSLSL

SRTNILVLDPANLAGLHSLRFLFLDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNLTAVPRGLPPSLEYL
LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSHLNHLEGLVLKDSSLYNLN
PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPSFGSLLSLQQLDMHGIF
FRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS
GDLALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQV
LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL
RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSLVL
LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG
TLKVLDVTGNPLHCACGAAFVDFLLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGLSLLT
VALGLAVPMLHHLCGWDLWYCFHLCLAWLPRRGRRRGADALPYDAFVVFDKAQSAVADWVYNELRVRLEERRGRR
ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILRPDAHR
SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFCRGPTTAE

SEQ ID NO:26 (Feline TLR9)

MGPCHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI
HHLHDSDFVHLSSLRRLNLKWNCPPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLVSLSL
SRTNILVLDPANLAGLHSLRFLFLDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNLTAVPRGLPPSLEYL
LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSHLNHLEGLVLKDSSLYNLN
PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPSFGSLLSLQQLDMHGIF
FRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS
GDLALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQV
LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL
RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSLVL
LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG
TLKVLDVTGNPLHCACGAAFVDFLLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG

SEQ ID NO:27 (Feline TLR9)

agggtctgcgagctccaggcattcttctctgccatcgctgcccagtctgccatccagaccctctggagaagcccc
cactccctgtcatgggcccctgccatggcgccctgcacccccctgtctctcctggtgcaggctgccgcgctggccg
tggccctggcccagggcaccctgcctgcctttctgccctgtgagctccagcgccacggcctggtgaattgcgact
ggctgttcctcaagtccgtgccccacttctcggcggcagcgccccgtggtaacgtcaccagcctttccctgtact
ccaaccgcatccaccacctccacgactccgactttgtccacctgtccagcctgcggcgtctcaacctcaaatgga
actgcccacccgccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttcctggccg
tgcccaccctggaggagctgaacctgagctacaacagcatcacgacagtacccgccctgcccagttccctcgtgt
ccctgtccttgagccgtaccaacatcctggtgctggaccctgccaacctcgcagggctgcactccctgcgctttc
tgttcctggatggcaactgctactacaagaacccctgcccgcaggccctgcaggtggccccgggcgccctccttg
gcctgggcaaccttacgcacctgtcactcaagtacaacaacctcactgcggtgccccgcggcctgcccccccagcc
tggagtacctgctattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgccctgc
gtgtgctcgatgtgggtgggaactgccgtcgctgtgaccacgcccgcaacccctgtatggagtgccccaagggct
tcccgcacctgcaccctgacaccttcagccacctgaaccacctcgaaggcctggtgttgaaggacagctctctct
acaacctgaaccccagatggttccatgccctgggcaacctcatggtgctggacctgagtgagaacttcctatatg
actgcatcaccaaaaccacagccttccagggcctggcccagctgcgcagactcaacttgtctttcaattaccaca
agaaggtgtcctttgcccacctgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatgc
atggcatcttcttccgctcgctcagcgagaccacgctccggtcgctggtccacctgcccatgctccagagtctgc
acctgcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc
tgtcagacaaccgcataagtggagccatggagctggcggctgccacgggggaggtggatggtggggagagagtcc
ggctgccatctggggacctagctctgggcccaccgggcacccctagctccgagggcttcatgccaggctgcaaga
ccctcaacttcaccttggacctgtcacggaacaacctagtgacaatccagccagagatgtttgcccggctctcgc
gcctccagtgcctgctcctgagccgcaacagcatctcgcaggcagtcaacggctcacaatttatgccgctgacca
gcctgcaggtgctggacctgtcccataacaagctggacctgtaccatgggcgctctttcacggagctgccgcggc
tggaggccctggacctcagctacaacagccagcccttcagcatgcagggcgtgggtcacaacctcagctttgtgg
cacagctgccggccctgcgctatctcagcctggcgcacaacgacatccacagccgtgtgtcccagcagctctgca
gcgcctcgctgcgggccttggacttcagcggcaatgccttgagccggatgtgggccgagggagacctgtatctcc
acttcttccgaggcctgaggagcctggtccggttggatctgtcccagaatcgcctgcataccctcttgccacgca
ccctggacaacctccccaagagcctgcggctgctgcgtctccgtgacaattatctggctttcttcaactggagca

gcctggtcctcctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagct
tgcctaatggaacccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagctttttg
ctctggccaccaggctgcgagagctcaacctcagtgccaacgccctcaagacggtggagccctcctggttcggtt
ctctagcgggcaccctgaaagtcctagatgtgactggcaacccctgcactgcgcctgtggggcggccttcgtgg
acttcttgctggaggtgcaggctgcagtgcccggcctgccaggccacgtcaagtgtggcagtccaggtcagctcc
agggccgcagcatctttgcgcaggatctgcgcctctgcctggatgaggccctctcctgggactgttttggcctct
cgctgctgaccgtggccctggcctggccgtgcccatgctgcaccacctctgtggctgggacctctggtactgct
tccacctgtgcctggcctggctgccccggcgggggcggcggcggggcgcggatgccctgccctacgatgcctttg
tggtcttcgacaaggcacagagcgcggtggccgactgggtgtacaacgagctgcgggtacggctagaggagcgcc
gtggacgccgagcgctccgcctgtgcctggaggaacgtgactggctacccggtaaaacgctctttgagaacctgt
gggcctcagtttacagcagccgcaagatgctgtttgtgctggcccacacagacagggtcagcggcctcttgcgcg
ccagctttctgctggcccagcagcgcctgctggaggaccgcaaggacgttgtggtgctggtgatcctgcgccccg
acgcccaccgctcccgctatgtgcggctgcgccagcgcctctgccgccagagcgtcctcctctggccccaccagc
ccagtggccagcgcagcttctgggcccagctgggcacggccctgaccagggacaaccagcacttctataaccaga
acttctgccggggccccacgacggcagagtgaccgcccagcaccccaagcctcctacaccttgcctgtctgcctg
ggatgccggg

SEQ ID NO:28 (Feline TLR9)

atgggcccctgccatggcgccctgcacccccctgtctctcctggtgcaggctgccgcgctggccgtggccctggcc
cagggcaccctgcctgcctttctgccctgtgagctccagcgccacggcctggtgaattgcgactggctgttcctc
aagtccgtgccccacttctcggcggcagcgccccgtggtaacgtcaccagcctttccctgtactccaaccgcatc
caccacctccacgactccgactttgtccacctgtccagcctgcggcgtctcaacctcaaatggaactgcccaccc
gccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttcctggccgtgcccaccctg
gaggagctgaacctgagctacaacagcatcacgacagtacccgccctgcccagttccctcgtgtccctgtccttg
agccgtaccaacatcctggtgctggaccctgccaacctcgcagggctgcactccctgcgctttctgttcctggat
ggcaactgctactacaagaacccctgcccgcaggccctgcaggtggccccgggcgccctccttggcctgggcaac
cttacgcacctgtcactcaagtacaacaacctcactgcggtgccccgcggcctgccccccagcctggagtacctg
ctattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgccctgcgtgtgctcgat
gtgggtgggaactgccgtcgctgtgaccacgcccgcaaccccctgtatggagtgccccaagggcttcccgcacctg
caccctgacaccttcagccacctgaaccacctcgaaggcctggtgttgaaggacagctctctctacaacctgaac
cccagatggttccatgccctgggcaacctcatggtgctggacctgagtgagaacttcctatatgactgcatcacc
aaaaccacagccttccagggcctggcccagctgcgcagactcaacttgtctttcaattaccacaagaaggtgtcc
tttgcccacctgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatgcatggcatcttc
ttccgctcgctcagcgagaccacgctccggtcgctggtccacctgcccatgctccagagtctgcacctgcagatg
aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgtcagacaac
cgcataagtggagccatggagctggcggctgccacgggggaggtggatggtggggagagagtccggctgccatct
ggggacctagctctgggcccaccgggcacccctagctccgagggcttcatgccaggctgcaagaccctcaacttc
accttggacctgtcacggaacaacctagtgacaatccagccagagatgtttgcccggctctcgcgcctccagtgc
ctgctcctgagccgcaacagcatctcgcaggcagtcaacggctcacaatttatgccgctgaccagcctgcaggtg
ctggacctgtcccataacaagctggacctgtaccatgggcgctctttcacggagctgccgcggctggaggccctg
gacctcagctacaacagccagcccttcagcatgcagggcgtgggtcacaacctcagctttgtggcacagctgccg
gccctgcgctatctcagcctggcgcacaacgacatccacagccgtgtgtcccagcagctctgcagcgcctcgctg
cgggccttggacttcagcggcaatgccttgagccggatgtgggccgagggagacctgtatctccacttcttccga
ggcctgaggagcctggtccggttggatctgtcccagaatcgcctgcataccctcttgccacgcaccctggacaac
ctccccaagagcctgcggctgctgcgtctccgtgacaattatctggctttcttcaactggagcagcctggtcctc
ctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgcctaatgga
acccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagctttttgctctggccacc
aggctgcgagagctcaacctcagtgccaacgccctcaagacggtggagccctcctggttcggttctctagcgggc
accctgaaagtcctagatgtgactggcaacccctgcactgcgcctgtggggcggccttcgtggacttcttgctg
gaggtgcaggctgcagtgcccggcctgccaggccacgtcaagtgtggcagtccaggtcagctccagggccgcagc
atctttgcgcaggatctgcgcctctgcctggatgaggccctctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

SEQ ID NO:29 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL
SHTNILVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTPGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDSSLHTLN
SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLSFNYRKKVSFARLHLASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRISGPSTLSEATPEEADDAEQEELL
SADPHPAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFSMKGIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLNSNS
VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLDNLPKSLKLLSLRDNYLSFFNWTSLS
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVRSNPLHCACGAAFVDLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLL
AVAVGMVVPILHHLCGWDVWYCFHLCLAWLPLLARSRRSAQALPYDAFVVFDKAQSAVADWVYNELRVRLEERRG
RRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDRVSGLLRTSFLLAQQRLLEDRKDVVVLVILRPDA
HRSRYVRLRQRLCRQSVLFWPQQPNGQGGFWAQLSTALTRDNRHFYNQNFCRGPTAE

SEQ ID NO:30 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL
SHTNILVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTPGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDSSLHTLN
SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLSFNYRKKVSFARLHLASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRISGPSTLSEATPEEADDAEQEELL
SADPHPAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFSMKGIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLNSNS
VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLDNLPKSLKLLSLRDNYLSFFNWTSLS
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVRSNPLHCACGAAFVDLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

SEQ ID NO:31 (Murine TLR9)

tgtcagagggagcctcgggagaatcctccatctcccaacatggttctccgtcgaaggactctgcaccccttgtcc
ctcctggtacaggctgcagtgctggctgagactctggccctgggtaccctgcctgccttcctaccctgtgagctg

aagcctcatggcctggtggactgcaattggctgttcctgaagtctgtaccccgtttctctgcggcagcatcctgc
tccaacatcacccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc
aacctgcggcagctgaacctcaagtggaactgtccacccactggccttagcccctgcacttctcttgccacatg
accattgagcccagaaccttcctggctatgcgtacactggaggagctgaacctgagctataatggtatcaccact
gtgccccgactgcccagctccctggtgaatctgagcctgagccacaccaacatcctggttctagatgctaacagc
ctcgccggcctatacagcctgcgcgttctcttcatggacgggaactgctactacaagaacccctgcacaggagcg
gtgaaggtgaccccaggcgccctcctgggcctgagcaatctcacccatctgtctctgaagtataacaacctcaca
aaggtgccccgccaactgcccccccagcctggagtacctcctggtgtcctataacctcattgtcaagctggggcct
gaagacctggccaatctgacctcccttcgagtacttgatgtgggtgggaattgccgtcgctgcgaccatgcccccc
aatccctgtatagaatgtggccaaaagtccctccacctgcaccctgagaccttccatcacctgagccatctggaa
ggcctggtgctgaaggacagctctctccatacactgaactcttcctggttccaaggtctggtcaacctctcggtg
ctggacctaagcgagaactttctctatgaaagcatcaaccacaccaatgcctttcagaacctaacccgcctgcgc
aagctcaacctgtccttcaattaccgcaagaaggtatcctttgcccgcctccacctggcaagttccttcaagaac
ctggtgtcactgcaggagctgaacatgaacggcatcttcttccgctcgctcaacaagtacacgctcagatggctg
gccgatctgcccaaactccacactctgcatcttcaaatgaacttcatcaaccaggcacagctcagcatctttggt
accttccgagcccttcgctttgtggacttgtcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc
cctgaagaggcagatgatgcagagcaggaggagctgttgtctgcggatcctcacccagctccactgagcacccct
gcttctaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctggtgact
atcaagccagagatgtttgtcaatctctcacgcctccagtgtcttagcctgagccacaactccattgcacaggct
gtcaatggctctcagttcctgccgctgactaatctgcaggtgctggacctgtcccataacaaactggacttgtac
cactggaaatcgttcagtgagctaccacagttgcaggccctggacctgagctacaacagccagccctttagcatg
aagggtataggccacaatttcagttttgtggcccatctgtccatgctacacagccttagcctggcacacaatgac
attcatacccgtgtgtcctcacatctcaacagcaactcagtgaggtttcttgacttcagcggcaacggtatgggc
cgcatgtgggatgagggggcctttatctccatttcttccaaggcctgagtggcctgctgaagctggacctgtct
caaaataacctgcatatcctccggccccagaaccttgacaacctccccaagagcctgaagctgctgagcctccga
gacaactacctatctttctttaactggaccagtctgtccttcctgcccaacctggaagtcctagacctggcaggc
aaccagctaaaggccctgaccaatggcaccctgcctaatggcaccctcctccagaaactggatgtcagcagcaac
agtatcgtctctgtggtcccagccttcttcgctctggcggtcgagctgaaagaggtcaacctcagccacaacatt
ctcaagacggtggatcgctcctggtttgggcccattgtgatgaacctgacagttctagacgtgagaagcaaccct
ctgcactgtgcctgtggggcagccttcgtagacttactgttggaggtgcagaccaaggtgcctggcctggctaat
ggtgtgaagtgtggcagccccggccagctgcagggccgtagcatcttcgcacaggacctgcggctgtgcctggat
gaggtcctctcttgggactgctttggcctttcactcttggctgtggccgtgggcatggtggtgcctatactgcac
catctctgcggctgggacgtctggtactgttttcatctgtgcctggcatggctacctttgctggcccgcagccga
cgcagcgcccaagctctcccctatgatgccttcgtggtgttcgataaggcacagagcgcagttgcggactgggtg
tataacgagctgcgggtgcggctggaggagcggcgcggtcgccgagccctacgcttgtgtctggaggaccgagat
tggctgcctggccagacgctcttcgagaacctctgggcttccatctatgggagccgcaagactctatttgtgctg
gcccacacggaccgcgtcagtggcctcctgcgcaccagcttcctgctggctcagcagcgcctgttggaagaccgc
aaggacgtggtggtgttggtgatcctgcgtccggatgcccaccgctcccgctatgtgcgactgcgccagcgtctc
tgccgccagagtgtgctcttctggccccagcagcccaacgggcagggggcttctgggcccagctgagtacagcc
ctgactagggacaaccgccacttctataaccagaacttctgccggggacctacagcagaatagctcagagcaaca
gctggaaacagctgcatcttcatgcctggttcccgagttgctctgcctgc

SEQ ID NO:31 (Murine TLR9)

atggttctccgtcgaaggactctgcaccccttgtccctcctggtacaggctgcagtgctggctgagactctggcc
ctgggtaccctgcctgccttcctaccctgtgagctgaagcctcatggcctggtggactgcaattggctgttcctg
aagtctgtaccccgtttctctgcggcagcatcctgctccaacatcacccgcctctccttgatctccaaccgtatc
caccacctgcacaactccgacttcgtccacctgtccaacctgcggcagctgaacctcaagtggaactgtccaccc
actggccttagcccctgcacttctcttgccacatgaccattgagcccagaaccttcctggctatgcgtacactg
gaggagctgaacctgagctataatggtatcaccactgtgccccgactgcccagctccctggtgaatctgagcctg
agccacaccaacatcctggttctagatgctaacagcctcgccggcctatacagcctgcgcgttctcttcatggac
gggaactgctactacaagaacccctgcacaggagcggtgaaggtgaccccaggcgccctcctgggcctgagcaat
ctcacccatctgtctctgaagtataacaacctcacaaaggtgccccgccaactgcccccccagcctggagtacctc
ctggtgtcctataacctcattgtcaagctggggcctgaagacctggccaatctgacctcccttcgagtacttgat
gtgggtgggaattgccgtcgctgcgaccatgcccccaatccctgtatagaatgtggccaaaagtccctccacctg
caccctgagaccttccatcacctgagccatctggaaggcctggtgctgaaggacagctctctccatacactgaac
tcttcctggttccaaggtctggtcaacctctcggtgctggacctaagcgagaactttctctatgaaagcatcaac
cacaccaatgcctttcagaacctaacccgcctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc

tttgcccgcctccacctggcaagttccttcaagaacctggtgtcactgcaggagctgaacatgaacggcatcttc
ttccgctcgctcaacaagtacacgctcagatggctggccgatctgcccaaactccacactctgcatcttcaaatg
aacttcatcaaccaggcacagctcagcatctttggtaccttccgagcccttcgctttgtggacttgtcagacaat
cgcatcagtgggccttcaacgctgtcagaagccacccctgaagaggcagatgatgcagagcaggaggagctgttg
tctgcggatcctcacccagctccactgagcacccctgcttctaagaacttcatggacaggtgtaagaacttcaag
ttcaccatggacctgtctcggaacaacctggtgactatcaagccagagatgtttgtcaatctctcacgcctccag
tgtcttagcctgagccacaactccattgcacaggctgtcaatggctctcagttcctgccgctgactaatctgcag
gtgctggacctgtcccataacaaactggacttgtaccactggaaatcgttcagtgagctaccacagttgcaggcc
ctggacctgagctacaacagccagccctttagcatgaagggtataggccacaatttcagttttgtggcccatctg
tccatgctacacagccttagcctggcacacaatgacattcatacccgtgtgtcctcacatctcaacagcaactca
gtgaggtttcttgacttcagcggcaacggtatgggccgcatgtgggatgagggggcctttatctccatttcttc
caaggcctgagtggcctgctgaagctggacctgtctcaaaataacctgcatatcctccggccccagaaccttgac
aacctccccaagagcctgaagctgctgagcctccgagacaactacctatctttctttaactggaccagtctgtcc
ttcctgcccaacctggaagtcctagacctggcaggcaaccagctaaaggccctgaccaatggcaccctgcctaat
ggcaccctcctccagaaactggatgtcagcagcaacagtatcgtctctgtggtcccagccttcttcgctctggcg
gtcgagctgaaagaggtcaacctcagccacaacattctcaagacggtggatcgctcctggtttgggcccattgtg
atgaacctgacagttctagacgtgagaagcaaccctctgcactgtgcctgtggggcagccttcgtagacttactg
ttggaggtgcagaccaaggtgcctggcctggctaatggtgtgaagtgtggcagccccggccagctgcagggccgt
agcatcttcgcacaggacctgcggctgtgcctggatgaggtcctctcttgggactgctttggc

SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI
HHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL
SHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL
LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLN
ASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIF
FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQP
GDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHF
LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS
ALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLA
VALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRG
RWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDG
RRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAE

SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI
HHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL
SHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL
LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLN
ASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIF
FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQP
GDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHF
LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS
ALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFA

SEQ ID NO:35 (Human TLR9)

aggctggtataaaaatcttacttcctctattctctgagccgctgctgcccctgtgggaagggacctcgagtgtga
agcatccttccctgtagctgctgtccagtctgcccgccagaccctctggagaagcccctgccccccagcatgggt
ttctgccgcagcgccctgcacccgctgtctctcctggtgcaggccatcatgctggccatgaccctggccctgggt

accttgcctgccttcctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttcctgaagtct
gtgccccacttctccatggcagcaccccgtggcaatgtcaccagcctttccttgtcctccaaccgcatccaccac
ctccatgattctgactttgcccacctgcccagcctgcggcatctcaacctcaagtggaactgcccgccggttggc
ctcagccccatgcacttcccctgccacatgaccatcgagcccagcaccttcttggctgtgcccaccctggaagag
ctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccaaatccctcatatccctgtccctcagccat
accaacatcctgatgctagactctgccagcctcgccggcctgcatgccctgcgcttcctattcatggacggcaac
tgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgccctccttggcctgggcaacctcacc
cacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctgctgttg
tcctacaaccgcatcgtcaaactggcgcctgaggacctggccaatctgaccgccctgcgtgtgctcgatgtgggc
ggaaattgccgccgctgcgaccacgctcccaacccctgcatggagtgccctcgtcacttcccccagctacatccc
gataccttcagccacctgagccgtcttgaaggcctggtgttgaaggacagttctctctcctggctgaatgccagt
tggttccgtgggctgggaaacctccgagtgctggacctgagtgagaacttcctctacaaatgcatcactaaaacc
aaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaaagagggtgtcctttgcc
cacctgtctctggccccttccttcgggagcctggtcgccctgaaggagctggacatgcacggcatcttcttccgc
tcactcgatgagaccacgctccggccactggcccgcctgcccatgctccagactctgcgtctgcagatgaacttc
atcaaccaggcccagctcggcatcttcagggccttccctggcctgcgctacgtggacctgtcggacaaccgcatc
agcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcctggggac
cttgctccggccccagtggacactcccagctctgaagacttcaggcccaactgcagcaccctcaacttcaccttg
gatctgtcacggaacaacctggtgaccgtgcagccggagatgtttgcccagctctcgcacctgcagtgcctgcgc
ctgagccacaactgcatctcgcaggcagtcaatggctcccagttcctgccgctgaccggtctgcaggtgctagac
ctgtcccgcaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctggacctc
agctacaacagccagccctttggcatgcagggcgtgggccacaacttcagcttcgtggctcacctgcgcaccctg
cgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctgcgggcc
ctggacttcagcggcaatgcactgggccatatgtggccgagggagacctctatctgcacttcttccaaggcctg
agcggtttgatctggctggacttgtcccagaaccgcctgcacaccctcctgccccaaaccctgcgcaacctcccc
aagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtggtggagcctccacttcctgccc
aaactggaagtcctcgacctggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggcacccgg
ctccggaggctggatgtcagctgcaacagcatcagcttcgtggcccccggcttcttttccaaggccaaggagctg
cgagagctcaaccttagcgccaacgccctcaagacagtggaccactcctggtttgggcccctggcgagtgccctg
caaatactagatgtaagcgccaaccctctgcactgcgcctgtggggcggcctttatggacttcctgctggaggtg
caggctgccgtgcccggtctgcccagccgggtgaagtgtggcagtccgggccagctccagggcctcagcatcttt
gcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgccctctcgctgctggctgtggct
ctgggcctgggtgtgcccatgctgcatcacctctgtggctgggacctctggtactgcttccacctgtgcctggcc
tggcttccctggcgggggcggcaaagtgggcgagatgaggatgccctgccctacgatgccttcgtggtcttcgac
aaaacgcagagcgcagtggcagactgggtgtacaacgagcttcgggggcagctggaggagtgccgtgggcgctgg
gcactccgcctgtgcctggaggaacgcgactggctgcctggcaaaaccctctttgagaacctgtgggcctcggtc
tatggcagccgcaagacgctgtttgtgctggcccacacggaccgggtcagtggtctcttgcgcgccagcttcctg
ctggcccagcagcgcctgctggaggaccgcaaggacgtcgtggtgctggtgatcctgagccctgacggccgccgc
tcccgctacgtgcggctgcgccagcgcctctgccgccagagtgtcctcctctggccccaccagcccagtggtcag
cgcagcttctgggcccagctgggcatggccctgaccagggacaaccaccacttctataaccggaacttctgccag
ggacccacggccgaatagccgtgagccggaatcctgcacggtgccacctccacactcacctcacctctgcctgcc
tggtctgaccctcccctgctcgcctccctcaccccacacctgacacagagca

SEQ ID NO:36 (Human TLR9)

atgggtttctgccgcagcgccctgcacccgctgtctctcctggtgcaggccatcatgctggccatgaccctggcc
ctgggtaccttgcctgccttcctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttcctg
aagtctgtgccccacttctccatggcagcaccccgtggcaatgtcaccagcctttccttgtcctccaaccgcatc
caccacctccatgattctgactttgcccacctgcccagcctgcggcatctcaacctcaagtggaactgcccgccg
gttggcctcagccccatgcacttcccctgccacatgaccatcgagcccagcaccttcttggctgtgcccaccctg
gaagagctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccaaatccctcatatccctgtccctc
agccataccaacatcctgatgctagactctgccagcctcgccggcctgcatgccctgcgcttcctattcatggac
ggcaactgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgccctccttggcctgggcaac
ctcacccacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctg
ctgttgtcctacaaccgcatcgtcaaactggcgcctgaggacctggccaatctgaccgccctgcgtgtgctcgat
gtgggcggaaattgccgccgctgcgaccacgctcccaacccctgcatggagtgccctcgtcacttcccccagcta
catcccgataccttcagccacctgagccgtcttgaaggcctggtgttgaaggacagttctctctcctggctgaat
gccagttggttccgtgggctgggaaacctccgagtgctggacctgagtgagaacttcctctacaaatgcatcact

```
aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaaagagggtgtcc
tttgcccacctgtctctggccccttccttcgggagcctggtcgccctgaaggagctggacatgcacggcatcttc
ttccgctcactcgatgagaccacgctccggccactggcccgcctgcccatgctccagactctgcgtctgcagatg
aacttcatcaaccaggcccagctcggcatcttcagggccttccctggcctgcgctacgtggacctgtcggacaac
cgcatcagcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcct
ggggaccttgctccggccccagtggacactcccagctctgaagacttcaggcccaactgcagcaccctcaacttc
accttggatctgtcacggaacaacctggtgaccgtgcagccggagatgtttgcccagctctcgcacctgcagtgc
ctgcgcctgagccacaactgcatctcgcaggcagtcaatggctcccagttcctgccgctgaccggtctgcaggtg
ctagacctgtcccgcaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctg
gacctcagctacaacagccagccctttggcatgcagggcgtgggccacaacttcagcttcgtggctcacctgcgc
accctgcgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctg
cgggccctggacttcagcggcaatgcactgggccatatgtggccgagggagacctctatctgcacttcttccaa
ggcctgagcggtttgatctggctggacttgtcccagaaccgcctgcacaccctcctgccccaaaccctgcgcaac
ctccccaagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtggtggagcctccacttc
ctgcccaaactggaagtcctcgacctggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggc
acccggctccggaggctggatgtcagctgcaacagcatcagcttcgtggcccccggcttcttttccaaggccaag
gagctgcgagagctcaaccttagcgccaacgccctcaagacagtggaccactcctggtttgggcccctggcgagt
gccctgcaaatactagatgtaagcgccaaccctctgcactgcgcctgtggggcggcctttatggacttcctgctg
gaggtgcaggctgccgtgcccggtctgcccagccgggtgaagtgtggcagtccgggccagctccagggcctcagc
atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc
```

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and nucleic acid molecules encoding them are provided by the invention. The chimeric polypeptides include at least one amino acid subsititution based on a comparison of conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine, equine, ovine, canine, feline, and human TLR9. The information contained in a multiple sequence alignment of these various TLR9 polypeptide sequences, provided for example in Figure 1, can be used to identify and select individual amino acid positions and even individual amino acids to substitute in designing a chimeric TLR9. The substitution or substitutions can be effected using methods known to those of ordinary skill in molecular biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino acid for a second amino acid, wherein side chains of the first amino acid and the second amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to alter conformation. For example, conservative amino acid substitutions generally may be made between members within each of the following groups: hydrophobic (A, I, L, M, V), neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-conservative amino acid substitution refers to any other amino acid substitution.

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, β-actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art. The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

Generally a nucleic acid coding sequence and a gene expression sequence are said to be "operably linked" when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be "operably linked" when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A "TLR9 ligand" as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

$$5'\text{-}N_1X_1CGX_2N_2\text{-}3'$$

wherein X_1 and X_2 are nucleotides, N is any nucleotide, and N_1 and N_2 are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments X_1 is adenine, guanine, or thymine and/or X_2 is cytosine, adenine, or thymine. In other embodiments X_1 is cytosine and/or X_2 is guanine.

Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the β-cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease). Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases. Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs, such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000) *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSELP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including κB kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF-κB. Examples of such promoters include, without limitation, those for NF-κB, IL-1β, IL-6, IL-8, IL-12 p40, CD80, CD86, and TNF-α. The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase, β-galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF-α). In certain embodiments the reporter is selected from IL-8, TNF-α, NF-κB-luciferase (NF-κB-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

Mol Cell Biol 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF-κB-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, IκB, NF-κB, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

Cells and Tissues. Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNA*later*™ (Ambion®, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

First-strand cDNA synthesis. Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using SUPERSCRIPT™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 μg of total RNA was added to 50 pmoles of oligo(dT) primer [poly $T_{(18)}$]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 μl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM $MgCl_2$) and 2 μl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERSCRIPT™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

PCR amplification. TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:
forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and
reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).
The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 μl contained 15 pmoles of each primer, 0.2 mM of dNTP mix and 1 μl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

Cloning and sequencing. The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZErO™ - 2

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

Results. Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

Example 2: Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, www.cmbi.kun.nl/bioinf/tools/clustalw.shtml). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in **Figure 1**. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clonetech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF-κB activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF-κB-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF-κB-luciferase reporter plasmid (NF-κB-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2μM, TCGTCGTTTTGTCGTTTTGTCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2μM, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF-κB activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF-κB-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2μM; TCCATGACGTTCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2μM;

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF-κB activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF-κB-luc reporter plasmid, 293 cells were transfected in 10 cm plates ($2x10^6$ cells/plate) with 16 μg of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF-κB-luciferase activity after stimulation with ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF-κB–luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF-κB–luciferase reporter
293-hTLR9:	expressing human TLR9
293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4: Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

$3x10^6$ 293T cells were electroporated with 5μg NF-κB-luc plasmid and 5 μg of either horse TLR9-pcDNA3.1 plasmid or humanTLR9-pcDNA3.1 plasmid at 200V, 975 μF. After the electroporation the cells were plated in 96-well cell culture plates at $2.5x10^4$ cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and frozen for at least 2 hours at –80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in **Figure 3.**

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:

aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;

generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identifed according to the method of any of claims 9 or 10.

12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:

contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;

measuring a signal in response to the contacting; and

identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF-κB.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF-κB.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

TCCATGACGTTTTGATGTT	(SEQ ID NO:39),
TCCATAACGTTTTGATGTT	(SEQ ID NO:40),
TCCATCACGTTTTGATGTT	(SEQ ID NO:41),
TCCATTACGTTTTGATGTT	(SEQ ID NO:42),
TCCATGGCGTTTTGATGTT	(SEQ ID NO:43),
TCCATGCCGTTTTGATGTT	(SEQ ID NO:44),
TCCATGTCGTTTTGATGTT	(SEQ ID NO:45),
TCCATGATGTTTTGATGTT	(SEQ ID NO:46),
TCCATGAAGTTTTGATGTT	(SEQ ID NO:47),
TCCATGAGGTTTTGATGTT	(SEQ ID NO:48),
TCCATGACATTTTGATGTT	(SEQ ID NO:49),
TCCATGACCTTTTGATGTT	(SEQ ID NO:50),
TCCATGACTTTTTGATGTT	(SEQ ID NO:51),
TCCATGACGCTTTGATGTT	(SEQ ID NO:52),
TCCATGACGATTTGATGTT	(SEQ ID NO:53),
TCCATGACGGTTTGATGTT	(SEQ ID NO:54),
TCCATGACGTCTTGATGTT	(SEQ ID NO:55),
TCCATGACGTATTGATGTT	(SEQ ID NO:56), and
TCCATGACGTGTTGATGTT	(SEQ ID NO:57).

Figure 1
(1/3)

```
feline    MGPCHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAAA 60
canine    MGPCRGALHPLSLLVQAAALALALAQGTLPAFLPCELQPHGLVNCNWLFLKSVPRFSAAA 60
bovine    MGP-YCAPHPLSLLVQAAALAAALAEGTLPAFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
mouse     MGP-YCAPHPLSLLVQAAALAAALAEGTLPAFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
ovine     MGP-YCAPHPLSLLVQAAALAAALAQGTLPAFLPCELQPRGKVNCNWLFLKSVPRFSAGA 59
porcine   MGP-RCTLHPLSLLVQVTALAAALAQGRLPAFLPCELQPHGLVNCNWLFLKSVPHFSAAA 59
horse     MGPCHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 60
human     MGPCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAA 60
rat       MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAE 60
          *      : :*******.  ** :** * **.******: :* *:*:********:** .

feline    PRGNVTSLSLYSNRIHHLHDSDFVHLSSLRRLNLKWNCPPASLSPMHFPCHMTIEPHTFL 120
canine    PRGNVTSLSLYSNRIHHLHDYDFVHFVHLRRLNLKWNCPPASLSPMHFPCHMTIEPNTFL 120
bovine    PRANVTSLSLISNRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFL 119
mouse     PRANVTSLSLISNRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFL 119
ovine     PRANVTSLSLISNRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFL 119
porcine   PRANVTSLSLLSNRIHHLHDSDFVHLSSLRTLNLKWNCPPAGLSPMHFPCHMTIEPNTFL 119
horse     PRDNVTSLSLLSNRIHHLHDSDFAQLSNLQKLNLKWNCPPAGLSPMHFPCHMTIEPNTFL 120
human     PRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFL 120
rat       PRSNITSLSLIANRIHHLHNLDFVHLPNVRQLNLKWNCPPPGLSPLHFSCRMTIEPKTFL 120
          ** *:***** :*******: **.::  :: ********* .***:**.*:***** ***

feline    AVPTLEELNLSYNSITTVPALPSSLVSLSLSRTNILVLDPANLAGLHSLRFLFLDGNCYY 180
canine    AVPTLEDLNLSYNSITTVPALPSSLVSLSLSRTNILVLDPATLAGLYALRFLFLDGNCYY 180
bovine    AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
mouse     AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
ovine     AVPTLEELNLSYNGITTVPALPSSLVSLSLSRTSILVLGPTHFTGLHALRFLYMDGNCYY 179
porcine   AVPTLEELNLSYNSITTVPALPDSLVSLSLSRTNILVLDPTHLTGLHALRYLYMDGNCYY 179
horse     AVPTLEELNLSYNGITTVPALPSSLVSLILSRTNILQLDPTSLTGLHALRFLYMDGNCYY 180
human     AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCYY 180
rat       AMRMLEELNLSYNGITTVPRLPSSLTNLSLSHTNILVLDASSLAGLHSLRVLFMDGNCYY 180
          *:  **:******.*.*** **.**..*.**:*.**.*..: :.**::** *::******

feline    KNPCPQALQVAPGALLGLGNLTHLSLKYNNLTAVPRGLPPSLEYLLLSYNHIITLAPEDL 240
canine    KNPCQQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYLLLSYNHIITLAPEDL 240
bovine    MNPCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLLLSYNHIVTLAPEDL 239
mouse     MNPCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLLLSYNHIVTLAPEDL 239
ovine     KNPCQQAVEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLLLSYNHIITLAPEDL 239
porcine   KNPCQGALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLLLSYNHIVTLTPEDL 239
horse     KNPCGRALEVAPGALLGLGNLTHLSLKYNNLTTVPRSLPPSLEYLLLSYNHIVTLAPEDL 240
human     KNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDL 240
rat       KNPCNGAVNVTPDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYLLLSYNLIVKLGAEDL 240
           ***   *:.*.*.*:***.************* *** **.**: ****** *:.* .***

feline    ANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSHLNHLEGLVLKDSSLYNLN 300
canine    ANLTALRVLDVGGNCRRCDHARNPCRECPKGFPQLHPNTFGHLSHLEGLVLRDSSLYSLD 300
bovine    ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLE 299
mouse     ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLE 299
ovine     ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLE 299
porcine   ANLTALRVLDVGGNCRRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSSLYNLD 299
horse     ANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN 300
human     ANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLN 300
rat       ANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSSLHSLN 300
          ****:**:*************  : * ** :  ..**.:** **.:******:****   *:

feline    PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPSF 360
canine    PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSF 360
bovine    KDWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSF 359
mouse     KDWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSF 359
ovine     KDWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFNYHKKVSFAHLQLAPSF 359
porcine   TRWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRSLNLSFNYHKKVSFAHLHLAPSF 359
horse     PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSF 360
human     ASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSF 360
rat       SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHLASSF 360
            **:.*  .* **********. *.**. *  .*::** *:***** *:****:* **.**
```

Figure 1
(2/3)

```
feline    GSLLSLQQLDMHGIFFRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPGLRYV 420
canine    GSLLSLQELDIHGIFFRSLSKTTLQSLAHLPMLQRLHLQLNFISQAQLSIFGAFPGLRYV 420
bovine    GSLVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFV 419
mouse     GSLVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFV 419
ovine     GGLVSLEKLDMHGIFFRSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFV 419
porcine   GHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYV 419
horse     GSLLSLQELDMHGIFFRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYI 420
human     GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYV 420
rat       KSLVSLQELNMNGIFFRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFV 420
            * :*::*:::***** * : **: *. ** *: * **:***.**:*.:*  * .* ::

feline    DLSDNRISGAMELAAATGEVDG--GERVRLPSGDLALGPPGTPSSEGFMPGCKTLNFTLD 478
canine    DLSDNRISGAAEPAAATGEVEADCGERVWPQSRDLALGPLGTPGSEAFMPSCRTLNFTLD 480
bovine    DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
mouse     DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
ovine     DLSDNRISGAARPVAALGEVDS--GVEVWRWPRGLAPGPLAAVSAKDFMPSCN-LNFTLD 476
porcine   DLSDNRISGAARPVAITREVDG--RERVWLPSRNLAPRPLDTLRSEDFMPNCKAFSFTLD 477
horse     DLSDNRISGAVEPVATTGEVDG--GKKVWLTSRDLTPGPLDTPSSEDFMPSCKNLSFTLD 478
human     DLSDNRISGASELTATMGEADG--GEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLD 478
rat       DLSNNRISGPPTLSRVAPEKAD-EAEKGVPWPASLTPALPSTPVSKNFMVRCKNLRFTMD 479
          ***:*****.        *         .     . .*:       : · :: *   *   : **:*

feline    LSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG 538
canine    LSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNLRVLDLSHNKLDLYHG 540
bovine    LSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG 536
mouse     LSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLDLSYNKLDLYHG 536
ovine     LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG 536
porcine   LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG 537
horse     LSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQVLDLSHNKLDLYHG 538
human     LSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHE 538
rat       LSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLKVLDLSYNKLDLYHS 539
          ******:**: :****.* :*:**:***:*****************:***:******** 

feline    RSFTELPRLEALDLSYNSQPFSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA 598
canine    RSFTELPRLEALDLSYNSQPFSMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA 600
bovine    RSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSA 596
mouse     RSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSA 596
ovine     RSFTELPQLEALDLSYNSQPFSMQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSA 596
porcine   RSFTELPRLEALDLSYNSQPFTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA 597
horse     RSFTELPRLEALDLSYNSQPFSMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCST 598
human     HSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCST 598
rat       KSFSELPQLQALDLSYNSQPFSMQGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYST 599
          :**:***:*:*********** *:*:***:**:*:*  *: ******.***:**.:* *:

feline    SLRALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLDNLPKSLRLL 658
canine    SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLL 660
bovine    SLRALDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQL 656
mouse     SLRALDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQL 656
ovine     SLRALDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQL 656
porcine   SLCALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHLHTLLPRALDNLPKSLKHL 657
horse     SLWALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLL 658
human     SLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVL 658
rat       SVEYLDFSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSQNKLHILRPQNLNYLPKSLTKL 659
          *:  ****** :.:** * **** **:.* .*: ****:*:** * *  *  *****  *

feline    RLRDNYLAFFNWSSLVLLPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSSNSISFVAS 718
canine    RLRDNYLAFFNWSSLALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVP 720
bovine    RLRDNNLAFFNWSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP 716
mouse     RLRDNNLAFFNWSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP 716
ovine     RLRDNNLAFFNWSSLTVLPQLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTP 716
porcine   HLRDNNLAFFNWSSLTLLPKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNP 717
horse     RLRNNYLAFFNWSSLTLLPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVP 718
human     RLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAP 718
rat       SFRDNHLSFFNWSSLAFLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVP 719
           :*:* *:**:* ** .**.*. ****** ****:**:** *  *::**:* *** **  .
```

Figure 1
(3/3)

```
feline     SFFALATRLRELNLSANALKTVEPSWFGSLAGTLKVLDVTGNPLHCACGAAFVDFLLEVQ 778
canine     SFFALAVRLRELNLSANALKTVEPSWFGSLAGALKVLDVTANPLHCACGATFVDFLLEVQ 780
bovine     GFFVRATRLIELNLSANALKTVDPSWFGSLAGTLKILDVSANPLHCACGAAFVDFLLERQ 776
mouse      GFFVRATRLIELNLSANALKTVDPSWFGSLAGTLKILDVSANPLHCACGAAFVDFLLERQ 776
ovine      GFFVLANRLKELNLSANALKTVDPFWFGRLTETLNILDVSANPLHCACGAAFVDFLLEMQ 776
porcine    GFFALAKQLEELNLSANALKTVEPSWFGSMVGNLKVLDVSANPLHCACGATFVGFLLEVQ 777
horse      GFFALATRLRELNLSANALRTEEPSWFGFLAGSLEVLDVSANPLHCACGAAFVDFLLQVQ 778
human      GFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQ 778
rat        AFFALAVELKEVNLSHNILKTVDRSWFGPIVMNLTVLDVSSNPLHCACGAPFVDLLLEVQ 779
           .**   *  .* *:*** * *:*  :   ***  :.   *  :***:.*********.*:.:**: *

feline     AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGLSLLTVALGLAVPMLHHL 838
canine     AAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFSLSLLAVALSLAVPMLHQL 840
bovine     EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGLSLLMVALGLAVPMLHHL 836
mouse      EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGLSLLMVALGLAVPMLHHL 836
ovine      AAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSLDCFGFSLLMVALGLAVPMLHHL 836
porcine    AAVPGLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLSWNCFGISLLAMALGLVVPMLHHL 837
horse      AAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLVVALGLAMPMLHHL 838
human      AAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHL 838
rat        TKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLLAVAVGTVLPLLQHL 839
             ****.  *.**** **** ***:********. **  **.:*** :*:.  :*:*:*:*

feline     CGWDLWYCFHLCLAWLPRRGRR--RGADALPYDAFVVFDKAQSAVADWVYNELRVRLEER 896
canine     CGWDLWYCFHLCLAWLPRRGRR--RGVDALAYDAFVVFDKAQSSVADWVYNELRVQLEER 898
bovine     CGWDLWYCFHLCLAHLPRRRRQ--RGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEER 894
mouse      CGWDLWYCFHLCLAHLPRRRRQ--RGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEER 894
ovine      CGWDLWYCFHLCLAHLPRRRRQ--RGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEER 894
porcine    CGWDLWYCFHLCLAWLPHRGQR--RGADALFYDAFVVFDKAQSAVADWVYNELRVQLEER 895
horse      CGWDLWYCFHLGLAWLPRRGWQ--RGADALSYDAFVVFDKAQSAVADWVYNELRVRLEER 896
human      CGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEEC 898
rat        CGWDVWYCFHLCLAWLPLLTRGR-RSAQALPYDAFVVFDKAQSAVADWVYNELRVRLEER 898
           ****:****** ** **        *. ::* ***.*****.**:**********  :***

feline     RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRL 956
canine     RGRRALRLCLEERDWVPGKTLFENLWASVYSSRKTLFVLARTDRVSGLLRASFLLAQQRL 958
bovine     RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRL 954
mouse      RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRL 954
ovine      RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRL 954
porcine    RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRL 955
horse      RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRL 956
human      RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRL 958
rat        RGRRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRL 958
           *** *******:***:**:**********:*.*** :*** :**:******:*********

feline     LEDRKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQ 1016
canine     LEDRKDVVVLVILCPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNR 1018
bovine     LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNR 1014
mouse      LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNR 1014
ovine      LEDRKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNR 1014
porcine    LEDRKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNH 1015
horse      LEDRKDVVVLVILSPDARRSRYVRLRQRLCRQSVLFWPHQPSGQRSFWAQLGMALTRDNR 1016
human      LEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNH 1018
rat        LEDRKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLFWPHQPNGQGSFWAQLSTALTRDNH 1018
           ************* *  . *****************:***** ** ****:*. ******:

feline     HFYNQNFCRGPTTAE------------------------------------------ 1031
canine     HFYNQNFCRGPTTA------------------------------------------- 1032
bovine     HFYNRNFCRGPTTAE------------------------------------------ 1029
mouse      HFYNRNFCRGPTTAE------------------------------------------ 1032
ovine      HFYNRNFCRGPTTAE------------------------------------------ 1029
porcine    HFYNRNFCRGPTTAE------------------------------------------ 1030
horse      HFYNQNFCRGPTMAE------------------------------------------ 1031
human      HFYNRNFCQGPTAE------------------------------------------- 1032
rat        HFYNRNFCRGPTAE------------------------------------------- 1032
           ****:***:***
```

Figure 2

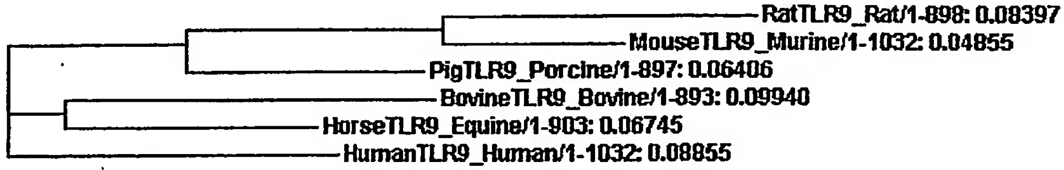
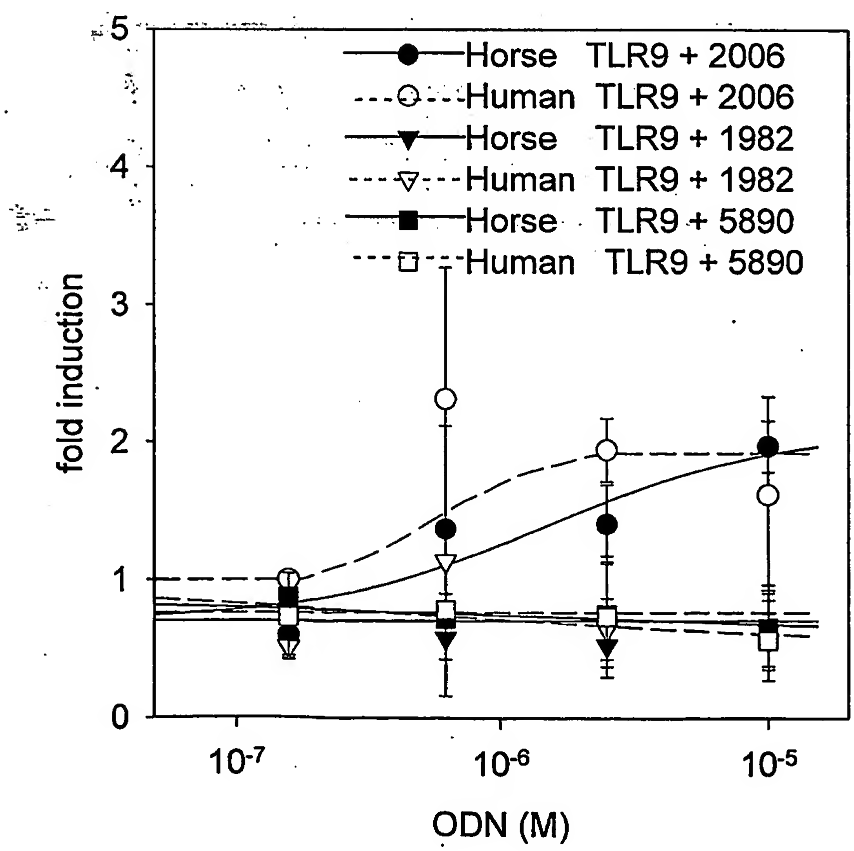


Figure 3



SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH
University of Saskatchewan
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479
<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1
<211> 1032
<212> PRT
<213> Rattus norvegicus

<400> 1

```
Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1               5                   10                  15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
            20                  25                  30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
        35                  40                  45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
    50                  55                  60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65                  70                  75                  80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
                85                  90                  95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
            100                 105                 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
        115                 120                 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
    130                 135                 140
```

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
805 810 815

Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val
820 825 830

Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln
995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
1025 1030

<210> 2
<211> 821
<212> PRT
<213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
805 810 815

Arg Asp Cys Phe Gly
820

<210> 3
<211> 3099
<212> DNA
<213> Rattus norvegicus

<400> 3
atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtacaggc cgcagtgctg 60

gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120

ggcctggtag actgcaactg gctcttcctg aagtctgtgc ctcacttctc tgccgcagaa 180

ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240

ctcgactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300

cctggcctca gccccttgca cttctcctgc cgcatgacca ttgagcccaa aaccttcctg 360

gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420

ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480

agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540

aagaacccct gcaacggggc ggtgaacgtg accccggacg ccttcctggg cttgagcaac 600

ctcacccact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660

agcctggagt acctcctgct gtcctataac ctcatcgtca agctgggggc cgaagaccta 720

gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780

gcccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc 840
catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctcgctgaac 900
tccaagtggt tccagggtct ggcgaacctc tcggtgctgg acctaagcga gaactttctc 960
tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020
ctgtccttca attactgcaa gaaggtatcg ttcgcccgcc tccacctggc aagttccttc 1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctggtctg cccaagctcc acacgctgca ccttcaaatg 1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc cccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccgagc 1380
actcccgtct caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cacgcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggt gtgggccgca tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaat 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gcccattgtg atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cggtgcaccc tttgtagact tactgctgga agtgcagacc 2340
aaggtgcctg gcctggctaa cggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460
ggcctttcac tcctggctgt ggccgtgggc acggtgttgc ctttactgca gcatctctgc 2520
ggctgggacg tctggtactg tttccatctg tgcctggcat ggctaccttt gctgacccgt 2580

ggccggcgca gcgcccaagc tctcccttat gatgccttcg tggtgttcga taaggcgcag 2640

agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700

cgccgagccc tacgcttgtg tctggaggac cgagattggc tgcctggcca gacactcttc 2760

gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttgtgct ggcccacacg 2820

gacaaggtca gtggcctcct gcgcaccagc ttcctgctgg ctcagcagcg cctgctggag 2880

gaccgcaagg acgtggtggt gttggtgatc ctgcgccctg atgcccaccg ctcccgctac 2940

gtgcgactgc gccagcgcct ctgccgccag agtgtgctct tctggcccca tcagcccaac 3000

gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060

tataaccgga acttctgccg ggacctaca gcagaatag 3099

<210> 4
<211> 2463
<212> DNA
<213> Rattus norvegicus

<400> 4
atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtacaggc cgcagtgctg 60

gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120

ggcctggtag actgcaactg gctcttcctg aagtctgtgc ctcacttctc tgccgcagaa 180

ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240

ctcgactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300

cctggcctca gccccttgca cttctcctgc cgcatgacca ttgagcccaa aaccttcctg 360

gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420

ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480

agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540

aagaacccct gcaacggggc ggtgaacgtg accccggacg ccttcctggg cttgagcaac 600

ctcacccact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660

agcctggagt acctcctgct gtcctataac ctcatcgtca agctgggggc cgaagaccta 720

gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780

gcccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc 840

catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctcgctgaac 900

tccaagtggt tccagggtct ggcgaacctc tcggtgctgg acctaagcga gaactttctc 960

tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020

```
ctgtccttca attactgcaa gaaggtatcg ttcgcccgcc tccacctggc aagttccttc   1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac   1140
aagaacacgc tcaggtggct ggctggtctg cccaagctcc acacgctgca ccttcaaatg   1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg   1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc cccgaaaag   1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccgagc   1380
actcccgtct caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg   1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag   1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg   1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa   1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc   1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac   1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cacgcctcta cagcacctca   1800
gtggagtatc tggacttcag cggcaacggt gtgggccgca tgtgggacga ggaggacctt   1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag   1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt   1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg   2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaat   2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc   2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact   2220
gtggatcgct cctggtttgg gcccattgtg atgaacctga cggttctaga cgtgagcagc   2280
aaccctctgc attgtgcctg cggtgcaccc tttgtagact tactgctgga agtgcagacc   2340
aaggtgcctg gcctggctaa cggtgtgaag tgtggcagtc cccgccagct gcagggccgc   2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt   2460
ggc                                                                 2463
```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu
725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys
740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr
755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro
770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile
785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn
805 810 815

Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro
820 825 830

Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu
835 840 845

Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala
850 855 860

Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val
865 870 875 880

Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg
885 890 895

Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro
900 905 910

Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg
915 920 925

Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu
930 935 940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg
965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp
980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr
995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys
1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu
1025 1030

<210> 6
<211> 819
<212> PRT
<213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
        355   360   365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
    370   375   380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
385   390   395   400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
                405   410   415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
            420   425   430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
        435   440   445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
    450   455   460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
465   470   475   480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
                485   490   495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
            500   505   510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
        515   520   525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
    530   535   540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
545   550   555   560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
                565   570   575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
            580   585   590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe
705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu
725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys
740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr
755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro
770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile
785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn
805 810 815

Cys Phe Gly

<210> 7
<211> 3352
<212> DNA
<213> Sus scrofa

<400> 7
gagcacgaac atccttcact gtagctgctg cccggtctgc cagccagacc ctttggagaa 60

gaccccactc cctgtcatgg gcccccgctg caccctgcac cccctttctc tcctggtgca 120

ggtgacagcg ctggctgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga 180

gctccagccc cacggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240

ctcggcggca gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300

ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360

gaactgcccg ccggctggcc tcagccccat gcacttcccc tgccacatga ccatcgagcc 420

caacaccttc ctggccgtgc ccaccctgga ggagctgaac ctgagctaca acagcatcac 480

gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct 540

ggtgctagac cccacccacc tcactggcct acatgccctg cgctacctgt acatggatgg 600

caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660

cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720

cagcctgccc cccagcctgg agaccctgct gttgtcctac aaccacattg tcaccctgac 780

gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg 840

ccgctgtgac catgcccgca acccctgcag ggagtgccca aaggaccacc ccaagctgca 900

ctctgacacc ttcagccacc tgagccgcct cgaaggcctg gtgttgaaag acagttctct 960

ctacaacctg gacaccaggt ggttccgagg cctggacagg ctccaagtgc tggacctgag 1020

tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact 1080

gcgcagcctc aacctgtcct tcaattacca caagaaggtg tcctttgccc acctgcacct 1140

ggcaccctcc tttgggcacc tccggtccct gaaggagctg gacatgcatg gcatcttctt 1200

ccgctcgctc agtgagacca cgctccaacc tctggtccaa ctgcctatgc tccagaccct 1260

gcgcctgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg ccttccctgg 1320

cctgctgtac gtggacctat cggacaaccg catcagcgga gctgcaaggc cagtggccat 1380

tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgctccacg 1440

tccactggac actctccgct cagaggactt catgccaaac tgcaaggcct tcagcttcac 1500

cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctcgcctctc 1560
acgcctcgag tgcctgcgcc tgagccacaa cagcatctcc caggcggtca atggctctca 1620
gtttgtgccg ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta 1680
tcacgggcgc tcgttcacgg agctgccgcg cctggaagca ctggacctca gctacaatag 1740
ccagcccttt accatgcagg gtgtgggcca caacctcagc ttcgtggccc agctgcccgc 1800
cctgcgctac ctcagcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg 1860
tagcgcctca ctgtgcgccc tggactttag cggcaacgat ctgagccgga tgtgggctga 1920
gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc 1980
ccagaaccac ctgcacaccc tcctgccacg tgccctggac aacctcccca aaagcctgaa 2040
gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgaccctcct 2100
gcccaagctg gaaaccctgg acttggctgg aaaccagctg aaggccctaa gcaatggcag 2160
cctgccatct ggcacccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt 2220
gaaccctggc ttctttgccc tggccaagca gttagaagag ctcaacctca gcgccaatgc 2280
cctcaagaca gtggagccct cctggtttgg ctcgatggtg ggcaacctga aagtcctaga 2340
cgtgagcgcc aaccctctgc actgtgcctg tggggcgacc ttcgtgggct tcctgctgga 2400
ggtacaggct gccgtgcctg ggctgcccag ccgcgtcaag tgtggcagtc cggggcagct 2460
ccagggccat agcatctttg cgcaagacct gcgcctctgc ctggatgaga ccctctcgtg 2520
gaactgtttt ggcatctcgc tgctggccat ggccctgggc ctggttgtgc ccatgctgca 2580
ccacctctgc ggctgggacc tctggtactg cttccacctg tgcctggcct ggctgcccca 2640
ccgagggcag cggcggggcg cagacgccct gttctatgat gccttcgtgg tctttgacaa 2700
agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg 2760
ccgtgggcgc cgcgcactgc gcctgtgcct ggaggagcga gactggttac ctggcaagac 2820
gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagaccctgt ttgtgctggc 2880
ccacacggac cgtgtcagcg gcctcttgcg tgccagtttc ctgctggccc agcagcgcct 2940
gctggaggac cgcaaggacg ttgtagtgct ggtgatcctg cgccccgatg cctaccgctc 3000
ccgctacgtg cggctgcgcc agcgcctctg ccgccagagt gtcctcctct ggccccacca 3060
gccccgtggg cagggcagct tctgggccca gctgggcaca gccctgacca gggacaacca 3120
ccacttctat aaccggaact tctgccgggg ccccacgaca gccgaatagc actgagtgac 3180
agcccagttg ccccagcccc cctggatttg cctctctgcc tggggtgccc caacctgctt 3240
tgctcagcca caccactgct ctgctccctg ttccccaccc cacccccag cctggcatgt 3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8
<211> 2457
<212> DNA
<213> Sus scrofa

<400> 8
atgggccccc gctgcaccct gcaccccctt tctctcctgg tgcaggtgac agcgctggct 60

gcggctctgg cccagggcag gctgcctgcc ttcctgccct gtgagctcca gccccacggc 120

ctggtgaact gcaactggct cttcctgaag tccgtgcccc acttctcggc ggcagcgccc 180

cgggccaacg tcaccagcct ctccttactc tccaaccgca tccaccacct gcacgactcc 240

gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaactg cccgccggct 300

ggcctcagcc ccatgcactt cccctgccac atgaccatcg agcccaacac cttcctggcc 360

gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgaccgt gcctgccctg 420

cccgactccc tcgtgtccct gtcgctgagc cgcaccaaca tcctggtgct agaccccacc 480

cacctcactg gcctacatgc cctgcgctac ctgtacatgg atggcaactg ctactacaag 540

aacccctgcc agggggcgct ggaggtggtg ccgggtgccc tcctcggcct gggcaacctc 600

acacatctct cactcaagta caacaatctc acggaggtgc cccgcagcct gccccccagc 660

ctggagaccc tgctgttgtc ctacaaccac attgtcaccc tgacgcctga ggacctggcc 720

aatctgactg ccctgcgcgt gcttgatgtg gggggggaact gccgccgctg tgaccatgcc 780

cgcaacccct gcagggagtg cccaaaggac caccccaagc tgcactctga caccttcagc 840

cacctgagcc gcctcgaagg cctggtgttg aaagacagtt ctctctacaa cctggacacc 900

aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa cttcctctac 960

gactgcatca ccaagaccac ggccttccag ggcctggccc gactgcgcag cctcaacctg 1020

tccttcaatt accacaagaa ggtgtccttt gcccacctgc acctggcacc ctcctttggg 1080

cacctccggt ccctgaagga gctggacatg catggcatct tcttccgctc gctcagtgag 1140

accacgctcc aacctctggt ccaactgcct atgctccaga ccctgcgcct gcagatgaac 1200

ttcattaacc aggcccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260

ctatcggaca accgcatcag cggagctgca aggccagtgg ccattactag ggaggtggat 1320

ggtagggaga gggtctggct gccttccagg aacctcgctc cacgtccact ggacactctc 1380

cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttgga cctgtctcgg 1440

aacaacctgg tgacaatcca gtcggagatg tttgctcgcc tctcacgcct cgagtgcctg 1500

cgcctgagcc acaacagcat ctcccaggcg gtcaatggct ctcagtttgt gccgctgacc 1560

agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620

acggagctgc cgcgcctgga agcactggac ctcagctaca atagccagcc ctttaccatg 1680

cagggtgtgg gccacaacct cagcttcgtg gcccagctgc ccgccctgcg ctacctcagc 1740

ctggcgcaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctcactgtgc 1800

gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860

cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920

accctcctgc cacgtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980

gacaataacc tggccttctt caactggagc agcctgaccc tcctgcccaa gctggaaacc 2040

ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100

cagctgcgga ggctggacct cagtggcaac agcatcggct ttgtgaaccc tggcttcttt 2160

gccctggcca agcagttaga agagctcaac ctcagcgcca atgccctcaa gacagtggag 2220

ccctcctggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaacccc 2280

ctgcactgtg cctgtggggc gaccttcgtg ggcttcctgc tggaggtaca ggctgccgtg 2340

cctgggctgc ccagccgcgt caagtgtggc agtccggggc agctccaggg ccatagcatc 2400

tttgcgcaag acctgcgcct ctgcctggat gagaccctct cgtggaactg ttttggc 2457

<210> 9
<211> 1029
<212> PRT
<213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln
370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro
420 425 430

Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg
930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala
995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 10
<211> 818
<212> PRT
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln
370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420 425 430

Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

```
Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
            660                 665                 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
        675                 680                 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
    690                 695                 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
705                 710                 715                 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
                725                 730                 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
            740                 745                 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
        755                 760                 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
    770                 775                 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785                 790                 795                 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
                805                 810                 815

Phe Gly
```

<210> 11
<211> 3191
<212> DNA
<213> Bos taurus

<400> 11

```
gggaagtggg cgccaagcat ccttccctgc agctgcctcc caacctgccc gccagaccct      60

ctggagaagc cgcattccct gtcatgggcc cctactgtgc cccgcacccc ctttctctcc     120

tggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttcctgc     180

cctgtgagct ccagccccat ggtcaggtgg actgcaactg gctgttcctg aagtctgtgc     240

cgcactttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc     300
```

gcatccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc 360
tcaagtggaa ctgcccgccg gccggcctca gccccatgca cttcccctgc cgtatgacca 420
tcgagcccaa caccttcctg gctgtgccca ccctggagga gctgaacctg agctacaacg 480
gcatcacgac cgtgcctgcc ctgcccagtt ccctcgtgtc cctgtcgctg agccacacca 540
gcatcctggt gctaggcccc acccacttca ccggcctgca cgccctgcgc tttctgtaca 600
tggacggcaa ctgctactac atgaacccct gcccgcgggc cctggaggtg gccccaggcg 660
ccctcctcgg cctgggcaac ctcacgcacc tgtcgctcaa gtacaacaac ctcacggagg 720
tgccccgccg cctgcccccc agcctggaca ccctgctgct gtcctacaac cacattgtca 780
ccctggcacc cgaggacctg gccaacctga ctgccctgcg cgtgcttgac gtgggtggga 840
actgccgccg ctgcgaccat gcccgcaacc cctgcaggga gtgcccaaag aacttcccca 900
agctgcaccc tgacaccttc agtcacctga gccgcctcga aggcctggtg ttgaaggaca 960
gttctctcta caaactagag aaagattggt tccgcggcct gggcaggctc caagtgctcg 1020
acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga 1080
cccagctgcg cagactcaac ctgtccttca attaccacaa gaaggtgtcc ttcgcccacc 1140
tgcacctagc gtcctccttt gggagtctgg tgtccctgga gaagctggac atgcacggca 1200
tcttcttccg ctccctcacc aacatcacgc tccagtcgct gacccggctg cccaagctcc 1260
agagtctgca tctgcagctg aacttcatca accaggccca gctcagcatc tttggggcct 1320
tcccgagcct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag 1380
cggccgccct gggggaggtg gacagcaggg tggaagtctg gcgattgccc aggggcctcg 1440
ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaagctgc aacctcaact 1500
tcaccttgga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttacccgcc 1560
tctcccgcct ccagtgcctg cgcctgagcc acaacagcat ctcgcaggcg gttaatggct 1620
cccagttcgt gccgctgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc 1680
tgtaccatgg gcgctcattc acggagctgc cgcagctgga ggcactggac ctcagctaca 1740
acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gcccagctgc 1800
cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc 1860
tcagcagcgc ctcgttgcgc gccctggact tcagcggcaa ctccctgagc cagatgtggg 1920
ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc 1980
tgtccgagaa ccatctgcac accctcctgc ctcgtcacct ggacaacctg cccaagagcc 2040

tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100

tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160

gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220

tcgtgatccc cggcttcttc gtccgcgcga ctcggctgat agagcttaac ctcagcgcca 2280

atgccctgaa gacagtggat ccctcctggt tcggttcctt agcagggacc ctgaaaatcc 2340

tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400

tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccgggcc 2460

agctccaggg ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520

ccttggactg ctttggcctc tcactgctaa tggtggcgct gggcctggca gtgcccatgc 2580

tgcaccacct ctgtggctgg gacctctggt actgcttcca cctgtgtctg gcccatttgc 2640

cccgacggcg gcggcagcgg ggcgaggaca ccctgctcta tgatgccgtc gtggtcttcg 2700

acaaggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760

agcgccgggg gcgccgggcg ctccgcctct gcctggagga gcgagactgg ctccctggta 2820

agacgctctt cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880

tggaccacac ggaccgggtc agcggcctcc tgcgcgccag cttcctgctg gcccagcagc 2940

gcctgttgga ggaccgcaag gacgtcgtag tgctggtgat cctgcgcccc gccgcctatc 3000

ggtcccgcta cgtgcggctg cgccagcgcc tctgccgcca gagcgtcctc ctctggcccc 3060

accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120

accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180

tgactgccca g 3191

<210> 12
<211> 2454
<212> DNA
<213> Bos taurus

<400> 12
atgggcccct actgtgcccc gcaccccctt tctctcctgg tgcaggcggc ggcactggca 60

gcggccctgg ccgagggcac cctgcctgcc ttcctgccct gtgagctcca gccccatggt 120

caggtggact gcaactggct gttcctgaag tctgtgccgc acttttcggc tggagccccc 180

cgggccaatg tcaccagcct ctccttaatc tccaaccgca tccaccactt gcatgactct 240

gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaactg cccgccggcc 300

ggcctcagcc ccatgcactt cccctgccgt atgaccatcg agcccaacac cttcctggct 360

gtgcccaccc tggaggagct gaacctgagc tacaacggca tcacgaccgt gcctgccctg 420
cccagttccc tcgtgtccct gtcgctgagc cacaccagca tcctggtgct aggccccacc 480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactacatg 540
aacccctgcc cgcgggccct ggaggtggcc ccaggcgccc tcctcggcct gggcaacctc 600
acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgccgcct gccccccagc 660
ctggacaccc tgctgctgtc ctacaaccac attgtcaccc tggcacccga ggacctggcc 720
aacctgactg ccctgcgcgt gcttgacgtg ggtgggaact gccgccgctg cgaccatgcc 780
cgcaacccct gcagggagtg cccaaagaac ttccccaagc tgcaccctga caccttcagt 840
cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa 900
gattggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa cttcctctat 960
gactacatca ccaagaccac catcttcaac gacctgaccc agctgcgcag actcaacctg 1020
tccttcaatt accacaagaa ggtgtccttc gcccacctgc acctagcgtc ctcctttggg 1080
agtctggtgt ccctggagaa gctggacatg cacggcatct tcttccgctc cctcaccaac 1140
atcacgctcc agtcgctgac ccggctgccc aagctccaga gtctgcatct gcagctgaac 1200
ttcatcaacc aggcccagct cagcatcttt ggggccttcc cgagcctgct cttcgtggac 1260
ctgtcggaca accgcatcag cggagccgcg acgccagcgg ccgccctggg ggaggtggac 1320
agcagggtgg aagtctggcg attgcccagg ggcctcgctc caggcccgct ggacgccgtc 1380
agctcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac 1440
aacctggtga caatccagca agagatgttt acccgcctct cccgcctcca gtgcctgcgc 1500
ctgagccaca acagcatctc gcaggcggtt aatggctccc agttcgtgcc gctgaccagc 1560
ctgcgagtgc tcgacctgtc ccacaacaag ctggacctgt accatgggcg ctcattcacg 1620
gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680
ggcgtgggcc acaacctcag cttcgtggcc cagctgccct ccctgcgcta cctcagcctt 1740
gcgcacaatg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gttgcgcgcc 1800
ctggacttca gcggcaactc cctgagccag atgtgggccg agggagacct ctatctctgc 1860
tttttcaaag gcttgaggaa cctggtccag ctggacctgt ccgagaacca tctgcacacc 1920
ctcctgcctc gtcacctgga caacctgccc aagagcctgc ggcagctgcg tctccgggac 1980
aataacctgg ccttcttcaa ctggagcagc ctgaccgtcc tgccccggct ggaagccctg 2040
gatctggcag gaaaccagct gaaggccctg agcaacggca gcctgccgcc tggcatccgg 2100
ctccagaagc tggacgtgag cagcaacagc atcggcttcg tgatccccgg cttcttcgtc 2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220

tcctggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caacccgctc 2280

cactgcgcct gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340

gggctgtcca ggcgcgtcac atgtggcagt ccgggccagc tccagggccg cagcatcttc 2400

acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13
<211> 1031
<212> PRT
<213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
385 390 395 400

```
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
                405                 410                 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
            420                 425                 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
        435                 440                 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
    450                 455                 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
465                 470                 475                 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
                485                 490                 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
            500                 505                 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
        515                 520                 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
    530                 535                 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545                 550                 555                 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
                565                 570                 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
            580                 585                 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
        595                 600                 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
    610                 615                 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
625                 630                 635                 640
```

```
His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
                645                 650                 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
            660                 665                 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
        675                 680                 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
    690                 695                 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
705                 710                 715                 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
                725                 730                 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
            740                 745                 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
        755                 760                 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
    770                 775                 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785                 790                 795                 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
                805                 810                 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met
            820                 825                 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
        835                 840                 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp
    850                 855                 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala
```

865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu
930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser
965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe
980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
995 1000 1005

Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe
1010 1015 1020

Cys Arg Gly Pro Thr Met Ala Glu
1025 1030

<210> 14
<211> 820
<212> PRT
<213> Equus caballus

<400> 14

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
740 745 750

```
Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
        755                 760                 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
    770                 775                 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785                 790                 795                 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
                805                 810                 815

Asp Cys Phe Gly
            820


&lt;210&gt;  15
&lt;211&gt;  3391
&lt;212&gt;  DNA
&lt;213&gt;  Equus caballus

&lt;400&gt;  15
ctctgttctc tgagctgttg ccgcgtgaag ggactgcgag cacaaagcat cctcctctgc      60

agctgctgcc cagtgtgcca gctggaccct ctggatcatc tcccactccc tgtcatgggc     120

ccttgccatg gtgccctgca gcccctgtct ctcctggtgc aggcggccat gctggccgtg     180

gctctggccc aaggcaccct gcctcccttc ctgccctgtg agctccagcc ccacggcctg     240

gtgaactgca actggctgtt cctgaagtcc gtgccccact tctcagcagc agcaccccgg     300

gacaatgtca ccagcctttc cttgctctcc aaccgcatcc accacctcca cgactccgac     360

tttgcccaac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc     420

ctcagcccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta     480

cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc     540

agctccctcg tgtccctgat cctgagccgc accaacatcc tgcagctaga ccccaccagc     600

ctcacgggcc tgcatgccct gcgcttccta tacatggatg gcaactgcta ctacaagaac     660

ccctgcgggc gggccctgga ggtggcccca ggcgccctcc ttggcctggg caacctcacc     720

cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg     780

gagtacctgc tgttgtccta caaccacatt gtcaccctgg cacctgagga cctggccaat     840

ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc     900

aacccctgcg tggagtgccc acataaattc cccagctgc actccgacac cttcagccac     960
```

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga 1020
tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac 1080
tgcatcacca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgtcc 1140
ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc 1200
ctgctctccc tgcaggaact ggacatgcat ggcatcttct tccgctcact cagccagaag 1260
acgctccagc cactggcccg cctgcccatg ctccagcgtc tgtatctgca gatgaacttc 1320
atcaaccagg cccagctcgg catcttcaag gacttccctg gtctgcgcta catagacctg 1380
tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt 1440
gggaagaagg tctggctgac atccagggac ctcactccag gcccactgga cacccccagc 1500
tctgaggact tcatgccaag ctgcaagaac ctcagcttca ccttggacct gtcacggaac 1560
aacctggtaa cagtccagcc agagatgttt gcccagctct cgcgcctcca gtgcctgcgc 1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc 1680
ctgcaggtgc tggacctgtc ccataacaaa ctggacctgt accatgggcg ctcgtttacg 1740
gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg 1800
ggtgtgggcc acaacctcag ctttgtggcc cagctgccca ccctgcgcta cctcagcctg 1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtgggcc 1920
ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc 1980
ttcttccaag gcctgagaag cctaatccgg ctagacctgt cccagaatcg tctgcatacc 2040
ctcctgccat gcaccctggg caacctcccc aagagcttgc agctgctgcg tctccgtaac 2100
aattacctgg ccttcttcaa ttggagcagc ctgaccctcc tgcccaacct ggaaaccctg 2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcacccag 2220
ctccagaggc tggacgtcag caggaacagc atcatcttcg tggtccctgg cttctttgct 2280
ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc 2340
tcctggtttg gtttcctagc aggctccctt gaagtcctag atgtgagcgc caaccctctg 2400
cactgcgcct gtggggcagc ctttgtggac ttcctgctgc aggttcaggc tgccgtgcct 2460
ggtctgccca gccgcgtcaa gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2520
gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggtctctca 2580
ttgctggttg tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac 2640
ctctggtact gcttccacct gggcctggcc tggctgcccc ggcgggggtg gcagcggggc 2700

gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760

gactgggtgt acaatgaact gcgggtgcgg ctagaggagc gccgtgggcg ccgggcgctc 2820

cgcctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880

gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940

ggcctcttgc gtgccagctt cctgctggcc cagcagcgtc tgctggagga ccgcaaggac 3000

gttgtggtgc tggtaatcct gagccctgac gcccgccgtt cccgttacgt gcggctgcgc 3060

cagcgcctct gccgccagag tgtcctcttc tggccccacc agcctagtgg ccagcgcagc 3120

ttctgggccc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180

ttctgccggg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaaccc 3240

ccagccctga ccttgcctct ctgcctatga tgcccagtct gcctcactct gtgacgcccc 3300

tgctctgcct ccgccaccct caccсctggc atacagcagg cactcaataa atgccactgg 3360

caggccaaac agccaaaaaa aaaaaaaaaa a 3391

<210> 16
<211> 2460
<212> DNA
<213> Equus caballus

<400> 16
atgggccctt gccatggtgc cctgcagccc ctgtctctcc tggtgcaggc ggccatgctg 60

gccgtggctc tggcccaagg caccctgcct cccttcctgc cctgtgagct ccagccccac 120

ggcctggtga actgcaactg gctgttcctg aagtccgtgc cccacttctc agcagcagca 180

ccccgggaca atgtcaccag cctttccttg ctctccaacc gcatccacca cctccacgac 240

tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaatggaa ctgcccgcca 300

gccggcctca gccccatgca cttcccctgc cacatgacca tcgagcccaa cactttcctg 360

gctgtaccca ccctggagga gctgaacctg agctacaacg gcatcacgac tgtgcctgcc 420

ctgcccagct ccctcgtgtc cctgatcctg agccgcacca acatcctgca gctagacccc 480

accagcctca cgggcctgca tgccctgcgc ttcctataca tggatggcaa ctgctactac 540

aagaacccct gcgggcgggc cctggaggtg gccccaggcg ccctccttgg cctgggcaac 600

ctcacccacc tgtcactcaa gtacaacaac ctcacaacgg tgccccgcag cctgcccccct 660

agcctggagt acctgctgtt gtcctacaac cacattgtca ccctggcacc tgaggacctg 720

gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgccg ctgtgaccat 780

gcacgcaacc cctgcgtgga gtgcccacat aaattccccc agctgcactc cgacaccttc 840

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac 900
cccagatggt tccgtggcct gggcaacctc acagtgctcg acctgagtga gaacttcctc 960
tacgactgca tcaccaaaac caaggcattc cagggcctgg cccagctgcg aagactcaac 1020
ttgtccttca attaccataa gaaggtgtcc ttcgcccacc tgacgctggc accctccttc 1080
gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttccg ctcactcagc 1140
cagaagacgc tccagccact ggcccgcctg cccatgctcc agcgtctgta tctgcagatg 1200
aacttcatca accaggccca gctcggcatc ttcaaggact tccctggtct gcgctacata 1260
gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg 1320
gatggtggga agaaggtctg gctgacatcc agggacctca ctccaggccc actggacacc 1380
cccagctctg aggacttcat gccaagctgc aagaacctca gcttcacctt ggacctgtca 1440
cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc 1500
ctgcgcctga gccacaacag catctcgcag gcggtcaatg gctcacagtt cgtgccactg 1560
accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg 1620
tttacggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
atgcggggtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgctacctc 1740
agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctgcag cacctcgctg 1800
tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat 1860
ctccgcttct tccaaggcct gagaagccta atccggctag acctgtccca gaatcgtctg 1920
catacccctcc tgccatgcac cctgggcaac ctccccaaga gcttgcagct gctgcgtctc 1980
cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa 2040
accctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc 2100
acccagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggt ccctggcttc 2160
tttgctctgg ccacgaggct gcgagagctc aacctcagtg ccaacgccct caggacagag 2220
gagccctcct ggtttggttt cctagcaggc tcccttgaag tcctagatgt gagcgccaac 2280
cctctgcact gcgcctgtgg ggcagccttt gtggacttcc tgctgcaggt tcaggctgcc 2340
gtgcctggtc tgcccagccg cgtcaagtgt ggcagtccgg gccagctcca gggccgcagc 2400
atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggt 2460

<210> 17
<211> 1029
<212> PRT
<213> Ovis aries

<400> 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala
995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 18
<211> 818
<212> PRT
<213> Ovis aries

<400> 18

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly

<210> 19
<211> 3199
<212> DNA
<213> Ovis aries

<400> 19
gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgccca acttgcccgc 60

cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgccc cgcacccccct 120

ttctctcctg gtgcaggcgg cggcgctggc agcagccctg gcccagggca ccctgcctgc 180

cttcctgccc tgtgagctcc agccccgggg taaggtgaac tgcaactggc tgttcctgaa 240

gtctgtgccg cgcttttcgg ccggagcccc ccgggccaat gtcaccagcc tctccttaat 300

ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcgggt 360

cctcaacctc aagtggaact gcccgccggc cggcctcagc cccatgcact tcccctgccg 420

catgaccatc gagcccaaca ccttcctggc tgtgcccacc ctggaggagc tgaacctgag 480

ctacaatggc atcacgaccg tgcctgccct gcccagttct ctcgtatccc tgtcgctgag 540

ccgcaccagc atcctggtgc taggccccac ccacttcacc ggcctgcacg ccctgcgctt 600

tctgtacatg gacggcaact gctactataa gaacccctgc cagcaggccg tggaggtggc 660

cccaggcgcc ctccttggcc tgggcaacct cacgcacctg tcgctcaagt acaacaacct 720

cacggaggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca 780

catcatcacc ctggcacccg aggacctggc caatctgact gccctgcgtg tgcttgatgt 840

gggcgggaac tgccgccgct gcgaccacgc ccgcaacccc tgcagggagt gcccaaagaa 900

cttccccaag ctgcaccctg acaccttcag ccacctgagc cgcctcgaag gcctggtgtt 960

gaaggacagt tctctctaca aactagagaa agactggttc cgcggcctgg gcaggctcca 1020

agtgctcgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag 1080

gaacctgacc cagctgcgca gactcaacct gtccttcaat taccacaaga aggtgtcctt 1140

cgcccacctg caactggcac cctcctttgg gggcctggtg tccctggaga agctggacat 1200

gcacggcatc ttcttccgct ccctcaccaa caccacgctc cggccgctga cccagctgcc 1260

caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt 1320

tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc 1380

gaggccggtg gccgccctcg ggaggtgga cagcggggtg gaagtctggc ggtggcccag 1440

gggcctcgct ccaggcccgc tggccgccgt cagcgcaaag gacttcatgc caagctgcaa 1500
cctcaacttc accttggacc tgtcacggaa caacctggtg acgatccagc aggagatgtt 1560
tacccgcctc tcccgcctcc agtgcctgcg cctgagccac aacagcatct cgcaggcggt 1620
taatggctcg cagttcgtgc cgctgacccg cctgcgagtg ctcgacctgt cctacaacaa 1680
gctggacctg taccatgggc gctcgttcac ggagctgccg cagctggagg cactggacct 1740
cagctacaac agccagccct tcagcatgca gggcgtgggc cacaacctca gcttcgtggc 1800
ccagctgccg tccctgcgct acctcagcct tgcgcacaac ggcatccaca gccgcgtgtc 1860
acagaagctc agcagcgcct cgctgcgcgc cctggacttc agcggcaact ccctgagcca 1920
gatgtgggcc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctggtcca 1980
gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc 2040
caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag 2100
cctgactgtt ctgccccagc tggaagccct ggatctggcg ggaaaccagc tgaaggccct 2160
gagcaacggc agcctgccac ctggcacccg gctccagaag ctggacgtga gcagcaacag 2220
catcggcttt gtgacccctg gcttctttgt ccttgccaac cggctgaaag agcttaacct 2280
cagcgccaac gccctgaaga cagtggatcc cttctggttc ggtcgcttaa cagagaccct 2340
gaatatccta gacgtgagcg ccaacccgct ccactgtgcc tgcggggcgg cctttgtgga 2400
cttcctgctg gagatgcagg cggccgtgcc tgggctgtcc aggcgcgtca cgtgtggcag 2460
tccgggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga 2520
gaccctctcc ttggactgct ttggcttctc gctgctaatg gtggcgctgg gcctggcggt 2580
gcccatgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc 2640
ccatttgccc cgacggcggc ggcagcgggg cgaggacacc ctgctctacg atgccttcgt 2700
ggtcttcgac aaggcgcaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca 2760
gctggaggag cgccgcgggc gccgggcgct ccgcctctgc ctggaggagc gagactggct 2820
ccctggcaag acgctcttcg agaacctgtg ggcctcggtc tacagcagcc gtaagaccat 2880
gttcgtgctg gaccacacgg accgggtcag tggcctcctg cgcgccagct tcctgctggc 2940
ccagcagcgc ctgttggagg accgcaagga tgtcgtggtg ctggtgatcc tgcgccccgc 3000
cgcctaccgg tcccgctacg tgcggctgcg ccagcgcctc tgccgccaga gcgtcctcct 3060
ctggccccac cagcccagtg gccagggtag cttctgggcc aacctgggca tggccctgac 3120
cagggacaac cgccacttct ataaccggaa cttctgccgg ggccccacga cagccgaata 3180

```
gcacagagtg actgcccag                                                3199

<210>  20
<211>  2454
<212>  DNA
<213>  Ovis aries

<400>  20
atgggcccct actgtgcccc gcaccccctt tctctcctgg tgcaggcggc ggcgctggca      60

gcagccctgg cccagggcac cctgcctgcc ttcctgccct gtgagctcca gccccggggt     120

aaggtgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagccccc     180

cgggccaatg tcaccagcct ctccttaatc tccaaccgca tccaccactt gcacgactct     240

gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaactg cccgccggcc     300

ggcctcagcc ccatgcactt cccctgccgc atgaccatcg agcccaacac cttcctggct     360

gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgccctg     420

cccagttctc tcgtatccct gtcgctgagc cgcaccagca tcctggtgct aggccccacc     480

cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag     540

aacccctgcc agcaggccgt ggaggtggcc ccaggcgccc tccttggcct gggcaacctc     600

acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgccgcct gcccccagc     660

ctggacaccc tgctgctgtc ctacaaccac atcatcaccc tggcacccga ggacctggcc     720

aatctgactg ccctgcgtgt gcttgatgtg ggcgggaact gccgccgctg cgaccacgcc     780

cgcaacccct gcagggagtg cccaaagaac ttccccaagc tgcaccctga caccttcagc     840

cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa     900

gactggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa cttcctctat     960

gactacatca ccaagaccac catcttcagg aacctgaccc agctgcgcag actcaacctg    1020

tccttcaatt accacaagaa ggtgtccttc gcccacctgc aactggcacc ctcctttggg    1080

ggcctggtgt ccctggagaa gctggacatg cacggcatct tcttccgctc cctcaccaac    1140

accacgctcc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac    1200

ttcatcaacc aggccgagct cagcatcttt ggggccttcc cgagcctgct cttcgtggac    1260

ctgtcggaca accgcatcag cggagctgcg aggccggtgg ccgccctcgg ggaggtggac    1320

agcggggtgg aagtctggcg gtggcccagg ggcctcgctc caggcccgct ggccgccgtc    1380

agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac    1440

aacctggtga cgatccagca ggagatgttt acccgcctct cccgcctcca gtgcctgcgc    1500
```

ctgagccaca acagcatctc gcaggcggtt aatggctcgc agttcgtgcc gctgacccgc 1560

ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620

gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680

ggcgtgggcc acaacctcag cttcgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740

gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gctgcgcgcc 1800

ctggacttca gcggcaactc cctgagccag atgtgggccg agggagacct ctatctctgc 1860

ttcttcaaag gcttgaggaa cctggtccag ctggacctgt ccaagaacca cctgcacacc 1920

ctcctgcctc gtcacctgga taacctgccc aagagcctgc ggcagctgcg tctccgggac 1980

aataacctgg ccttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040

gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcacccgg 2100

ctccagaagc tggacgtgag cagcaacagc atcggctttg tgacccctgg cttctttgtc 2160

cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220

ttctggttcg gtcgcttaac agagaccctg aatatcctag acgtgagcgc caacccgctc 2280

cactgtgcct gcggggcggc ctttgtggac ttcctgctgg agatgcaggc ggccgtgcct 2340

gggctgtcca ggcgcgtcac gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2400

gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21
<211> 1032
<212> PRT
<213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp
660 665 670

Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
675 680 685

Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
690 695 700

Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
705 710 715 720

Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
725 730 735

Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
740 745 750

Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
755 760 765

Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
770 775 780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu
820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys
835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly
850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala
1025 1030

<210> 22
<211> 822
<212> PRT
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

```
Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
        195                 200                 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
    210                 215                 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225                 230                 235                 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
                245                 250                 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
            260                 265                 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
        275                 280                 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
    290                 295                 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305                 310                 315                 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
                325                 330                 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
            340                 345                 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
        355                 360                 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
    370                 375                 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
385                 390                 395                 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
                405                 410                 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
            420                 425                 430
```

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro
545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660 665 670

Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
675 680 685

Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
690 695 700

Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
705 710 715 720

Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
725 730 735

Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
740 745 750

Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
755 760 765

Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
770 775 780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
805 810 815

Ser Trp Val Cys Phe Ser
820

<210> 23
<211> 3334
<212> DNA
<213> Canis familiaris

<400> 23
aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca 60

gaccctctgg agaagccccc gctccctgtc atgggcccct gccgtggcgc cctgcacccc 120

ctgtctctcc tggtgcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct 180

gccttcctgc cctgtgagct ccagccccat ggcctggtga actgcaactg gctgttcctc 240

aagtccgtgc cccgcttctc ggcagctgca ccccgcggta acgtcaccag cctttccttg 300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg 360

cgtctcaatc tcaagtggaa ctgcccgccc gccagcctca gccccatgca ctttccctgt 420

cacatgacca ttgagcccaa caccttcctg gctgtgccca ccctagagga cctgaatctg 480

agctataaca gcatcacgac tgtgcccgcc ctgcccagtt cgcttgtgtc cctgtccctg 540

agccgcacca acatcctggt gctggaccct gccaccctgg caggccttta tgccctgcgc 600

ttcctgttcc tggatggcaa ctgctactac aagaacccct gccagcaggc cctgcaggtg 660

gccccaggtg ccctcctggg cctgggcaac ctcacacacc tgtcactcaa gtacaacaac 720

ctcaccgtgg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtcctacaac 780

cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgtcctcgat 840

gtgggtggga actgtcgccg ctgtgaccat gcccgtaacc cctgcaggga gtgccccaag 900

ggcttccccc agctgcaccc caacaccttc ggccacctga gccacctcga aggcctggtg 960

ttgagggaca gctctctcta cagcctggac cccaggtggt tccatggcct gggcaacctc 1020

atggtgctgg acctgagtga gaacttcctg tatgactgca tcaccaaaac caaagccttc 1080

tacggcctgg cccggctgcg cagactcaac ctgtccttca attatcataa gaaggtgtcc 1140

tttgcccacc tgcatctggc atcctccttc gggagcctac tgtccctgca ggagctggac 1200

atacatggca tcttcttccg ctcgctcagc aagaccacgc tccagtcgct ggcccacctg 1260

cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc 1320

ttgggcgcct tccctggact gcggtacgtg gacttgtcag acaaccgcat cagtggagct 1380

gcagagcccg cggctgccac aggggaggta gaggcagact gtggggagag agtctggcca 1440

cagtcccggg accttgctct gggcccactg ggcacccccg gctcagaggc cttcatgccg 1500

agctgcagga ccctcaactt caccttggac ctgtctcgga acaacctagt gactgttcag 1560

ccggagatgt ttgtccggct ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc 1620

tcgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg 1680

tcccataaca agctggacct gtaccacggg cgctcgttca cggagctgcc gcggctggag 1740

gccttggacc tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc 1800

agctttgtgg cacagctgcc agccctgcgc tacctcagcc tggcgcacaa tggcatccac 1860

agccgcgtgt cccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat 1920

accctgagcc agatgtgggc cgagggagac ctctatctcc gcttcttcca aggcctgaga 1980

agcctggttc agctggacct gtcccagaat cgcctgcata ccctcctgcc acgcaacctg 2040

gacaacctcc ccaagagcct gcggctcctg cggctccgtg acaattacct ggctttcttc 2100

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160

ctgaaggccc tgagcaatgg cagcttgccc aacggcaccc agctccagag gctggacctc 2220

agcggcaaca gcatcggctt cgtggtcccc agctttttg ccctggccgt gaggcttcga 2280

gagctcaacc tcagcgccaa cgccctcaag acggtggagc cctcctggtt tggttccctg 2340

gcgggtgccc tgaaagtcct agacgtgacc gccaacccct tgcattgcgc ttgcggcgca 2400

accttcgtgg acttcttgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc 2460

aagtgcggca gcccgggcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520

tgcctggacg aagcgctctc ctgggtctgt ttcagcctct cgctgctggc tgtggccctg 2580

agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttccac 2640

ctgtgcctgg cctggctgcc ccggcggggg cggcggcggg gtgtggatgc cctggcctat 2700

gacgccttcg tggtcttcga caaggcgcag agctcggtgg cggactgggt gtacaatgag 2760

ctgcgggtac agctagagga gcgccgtggg cgccgggcgc tacgcctgtg tctggaggaa 2820

cgtgactggg tacccggcaa aaccctcttc gagaacctct gggcctcagt ttacagcagc 2880

cgcaagacgc tgtttgtgct ggcccgcacg gacagagtca gcggcctcct gcgtgccagc 2940

ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggt gctggtgatc 3000

ctgtgccccg acgcccaccg ctcccgctat gtgcggctgc gccagcgcct ctgccgccag 3060

agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc 3120

acggccctga ccagggacaa ccgccacttc tacaaccaga acttctgccg gggccccacg 3180

acagcctgat aggcagacag cccagcacct tcgcgcccct acaccctgcc tgtctgtctg 3240

ggatgcccga cctgctggct ctacaccgcc gctctgtctc ccctacaccc agccctggca 3300

taaagcgacc gctcaataaa tgctgctggt agac 3334

<210> 24
<211> 2466
<212> DNA
<213> Canis familiaris

<400> 24
atgggcccct gccgtggcgc cctgcacccc ctgtctctcc tggtgcaggc tgccgcgcta 60

gccctggccc tggcccaggg caccctgcct gccttcctgc cctgtgagct ccagccccat 120

ggcctggtga actgcaactg gctgttcctc aagtccgtgc cccgcttctc ggcagctgca 180

ccccgcggta acgtcaccag cctttccttg tactccaacc gcatccacca cctccatgac 240

tatgactttg tccacttcgt ccacctgcgg cgtctcaatc tcaagtggaa ctgcccgccc 300

gccagcctca gccccatgca ctttccctgt cacatgacca ttgagcccaa caccttcctg 360

gctgtgccca ccctagagga cctgaatctg agctataaca gcatcacgac tgtgcccgcc 420

ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggt gctggaccct 480

gccaccctgg caggccttta tgccctgcgc ttcctgttcc tggatggcaa ctgctactac 540

aagaacccct gccagcaggc cctgcaggtg gccccaggtg ccctcctggg cctgggcaac 600

ctcacacacc tgtcactcaa gtacaacaac ctcaccgtgg tgccgcgggg cctgcccccc 660

agcctggagt acctgctctt gtcctacaac cacatcatca ccctggcacc tgaggacctg 720

gccaatctga ctgccctgcg tgtcctcgat gtgggtggga actgtcgccg ctgtgaccat 780

gcccgtaacc cctgcaggga gtgccccaag ggcttccccc agctgcaccc caacaccttc 840

ggccacctga gccacctcga aggcctggtg ttgagggaca gctctctcta cagcctggac 900

cccaggtggt tccatggcct gggcaacctc atggtgctgg acctgagtga gaacttcctg 960

tatgactgca tcaccaaaac caaagccttc tacggcctgg cccggctgcg cagactcaac 1020

ctgtccttca attatcataa gaaggtgtcc tttgcccacc tgcatctggc atcctccttc 1080

gggagcctac tgtccctgca ggagctggac atacatggca tcttcttccg ctcgctcagc 1140

aagaccacgc tccagtcgct ggcccacctg cccatgctcc agcgtctgca tctgcagttg 1200

aactttatca gccaggccca gctcagcatc ttcggcgcct tccctggact gcggtacgtg 1260

gacttgtcag acaaccgcat cagtggagct gcagagcccg cggctgccac aggggaggta 1320

gaggcagact gtggggagag agtctggcca cagtcccggg accttgctct gggcccactg 1380

ggcacccccg gctcagaggc cttcatgccg agctgcagga ccctcaactt caccttggac 1440

ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcgcgcctc 1500

cagtgcctgg gcctgagcca caacagcatc tcgcaggcgg tcaatggctc gcagttcgtg 1560

cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccacggg 1620

cgctcgttca cggagctgcc gcggctggag gccttggacc tcagctacaa cagccagccc 1680

ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740

tacctcagcc tggcgcacaa tggcatccac agccgcgtgt cccagcagct ccgcagcgcc 1800

tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgagggagac 1860

ctctatctcc gcttcttcca aggcctgaga agcctggttc agctggacct gtcccagaat 1920

cgcctgcata ccctcctgcc acgcaacctg gacaacctcc ccaagagcct gcggctcctg 1980

cggctccgtg acaattacct ggctttcttc aactggagca gcctggccct cctacccaag 2040

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100

aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggctt cgtggtcccc 2160

agctttttg ccctggccgt gaggcttcga gagctcaacc tcagcgccaa cgccctcaag 2220

acggtggagc cctcctggtt tggttccctg gcgggtgccc tgaaagtcct agacgtgacc 2280

gccaacccct tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340

gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400

cgcagcatct tcgcacagga cctgcgcctc tgcctggacg aagcgctctc ctgggtctgt 2460

ttcagc 2466

<210> 25
<211> 1031
<212> PRT
<213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly Ala Asp
850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala
865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu
930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser
965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu
980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe
1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu
1025 1030

<210> 26
<211> 820
<212> PRT
<213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

```
Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
            20                  25                  30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
        35                  40                  45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
    50                  55                  60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65                  70                  75                  80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
                85                  90                  95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
            100                 105                 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
        115                 120                 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
    130                 135                 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145                 150                 155                 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
                165                 170                 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
            180                 185                 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
        195                 200                 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
    210                 215                 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225                 230                 235                 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
                245                 250                 255
```

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725 730 735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Gly
820

<210> 27
<211> 3235
<212> DNA
<213> Felis catus

<400> 27
agggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60
ctctggagaa gcccccactc cctgtcatgg gcccctgcca tggcgccctg cacccccctgt 120
ctctcctggt gcaggctgcc gcgctggccg tggccctggc ccagggcacc ctgcctgcct 180
ttctgccctg tgagctccag cgccacggcc tggtgaattg cgactggctg ttcctcaagt 240
ccgtgcccca cttctcggcg gcagcgcccc gtggtaacgt caccagcctt tccctgtact 300
ccaaccgcat ccaccacctc cacgactccg actttgtcca cctgtccagc ctgcggcgtc 360
tcaacctcaa atggaactgc ccacccgcca gcctcagccc catgcacttc ccctgtcaca 420
tgaccattga gccccacacc ttcctggccg tgcccaccct ggaggagctg aacctgagct 480
acaacagcat cacgacagta cccgccctgc ccagttccct cgtgtccctg tccttgagcc 540
gtaccaacat cctggtgctg gaccctgcca acctcgcagg gctgcactcc ctgcgctttc 600
tgttcctgga tggcaactgc tactacaaga acccctgccc gcaggccctg caggtggccc 660
cgggcgccct ccttggcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca 720
ctgcggtgcc ccgcggcctg ccccccagcc tggagtacct gctattgtcc tacaaccaca 780

```
tcatcaccct ggcacctgag gacctggcca acctgaccgc cctgcgtgtg ctcgatgtgg    840
gtgggaactg ccgtcgctgt gaccacgccc gcaacccctg tatggagtgc cccaagggct    900
tcccgcacct gcaccctgac accttcagcc acctgaacca cctcgaaggc ctggtgttga    960
aggacagctc tctctacaac ctgaacccca gatggttcca tgccctgggc aacctcatgg   1020
tgctggacct gagtgagaac ttcctatatg actgcatcac caaaaccaca gccttccagg   1080
gcctggccca gctgcgcaga ctcaacttgt ctttcaatta ccacaagaag gtgtcctttg   1140
cccacctgca tctggcgccc tccttcggga gcctgctctc cctgcagcag ctggacatgc   1200
atggcatctt cttccgctcg ctcagcgaga ccacgctccg gtcgctggtc cacctgccca   1260
tgctccagag tctgcacctg cagatgaact tcatcaatca ggcccagctc agcatcttcg   1320
gggccttccc tggcctgcga tacgtggacc tgtcagacaa ccgcataagt ggagccatgg   1380
agctggcggc tgccacgggg gaggtggatg gtggggagag agtccggctg ccatctgggg   1440
acctagctct gggcccaccg ggcaccccta gctccgaggg cttcatgcca ggctgcaaga   1500
ccctcaactt caccttggac ctgtcacgga acaacctagt gacaatccag ccagagatgt   1560
ttgcccggct ctcgcgcctc cagtgcctgc tcctgagccg caacagcatc tcgcaggcag   1620
tcaacggctc acaatttatg ccgctgacca gcctgcaggt gctggacctg tcccataaca   1680
agctggacct gtaccatggg cgctctttca cggagctgcc gcggctggag gccctggacc   1740
tcagctacaa cagccagccc ttcagcatgc agggcgtggg tcacaacctc agctttgtgg   1800
cacagctgcc aggccctgcgc tatctcagcc tggcgcacaa cgacatccac agccgtgtgt   1860
cccagcagct ctgcagcgcc tcgctgcggg ccttggactt cagcggcaat gccttgagcc   1920
ggatgtgggc cgagggagac ctgtatctcc acttcttccg aggcctgagg agcctggtcc   1980
ggttggatct gtcccagaat cgcctgcata ccctcttgcc acgcaccctg gacaacctcc   2040
ccaagagcct gcggctgctg cgtctccgtg acaattatct ggctttcttc aactggagca   2100
gcctggtcct cctccccagg ctggaagccc tggacctggc gggaaaccag ctgaaggccc   2160
tgagcaacgg cagcttgcct aatggaaccc agctccagag gctggacctc agcagcaaca   2220
gtatcagctt cgtggcctcc agcttttttg ctctggccac caggctgcga gagctcaacc   2280
tcagtgccaa cgccctcaag acggtggagc cctcctggtt cggttctcta gcgggcaccc   2340
tgaaagtcct agatgtgact ggcaaccccc tgcactgcgc ctgtggggcg gccttcgtgg   2400
acttcttgct ggaggtgcag gctgcagtgc ccggcctgcc aggccacgtc aagtgtggca   2460
gtccaggtca gctccagggc cgcagcatct ttgcgcagga tctgcgcctc tgcctggatg   2520
aggccctctc ctgggactgt tttggcctct cgctgctgac cgtggccctg ggcctggccg   2580
```

tgcccatgct gcaccacctc tgtggctggg acctctggta ctgcttccac ctgtgcctgg 2640

cctggctgcc ccggcggggg cggcggcggg gcgcggatgc cctgccctac gatgcctttg 2700

tggtcttcga caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760

ggctagagga gcgccgtgga cgccgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820

tacccggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880

tgtttgtgct ggcccacaca gacagggtca gcggcctctt gcgcgccagc tttctgctgg 2940

cccagcagcg cctgctggag gaccgcaagg acgttgtggt gctggtgatc ctgcgccccg 3000

acgcccaccg ctcccgctat gtgcggctgc gccagcgcct ctgccgccag agcgtcctcc 3060

tctggccccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc acggccctga 3120

ccagggacaa ccagcacttc tataaccaga acttctgccg ggccccacg acggcagagt 3180

gaccgcccag caccccaagc ctcctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28
<211> 2460
<212> DNA
<213> Felis catus

<400> 28
atgggcccct gccatggcgc cctgcacccc ctgtctctcc tggtgcaggc tgccgcgctg 60

gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120

ggcctggtga attgcgactg gctgttcctc aagtccgtgc cccacttctc ggcggcagcg 180

ccccgtggta acgtcaccag cctttccctg tactccaacc gcatccacca cctccacgac 240

tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaatggaa ctgcccaccc 300

gccagcctca gccccatgca cttcccctgt cacatgacca ttgagcccca caccttcctg 360

gccgtgccca ccctggagga gctgaacctg agctacaaca gcatcacgac agtacccgcc 420

ctgcccagtt ccctcgtgtc cctgtccttg agccgtacca acatcctggt gctggaccct 480

gccaacctcg cagggctgca ctccctgcgc tttctgttcc tggatggcaa ctgctactac 540

aagaacccct gcccgcaggc cctgcaggtg gccccgggcg ccctccttgg cctgggcaac 600

cttacgcacc tgtcactcaa gtacaacaac ctcactgcgg tgccccgcgg cctgcccccc 660

agcctggagt acctgctatt gtcctacaac cacatcatca ccctggcacc tgaggacctg 720

gccaacctga ccgccctgcg tgtgctcgat gtgggtggga actgccgtcg ctgtgaccac 780

gcccgcaacc cctgtatgga gtgccccaag ggcttcccgc acctgcaccc tgacaccttc 840

agccacctga accacctcga aggcctggtg ttgaaggaca gctctctcta caacctgaac 900

```
cccagatggt tccatgccct gggcaacctc atggtgctgg acctgagtga gaacttccta     960
tatgactgca tcaccaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac    1020
ttgtctttca attaccacaa gaaggtgtcc tttgcccacc tgcatctggc gccctccttc    1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttccg ctcgctcagc    1140
gagaccacgc tccggtcgct ggtccacctg cccatgctcc agagtctgca cctgcagatg    1200
aacttcatca atcaggccca gctcagcatc ttcggggcct tccctggcct gcgatacgtg    1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg    1320
gatggtgggg agagagtccg gctgccatct ggggacctag ctctgggccc accgggcacc    1380
cctagctccg agggcttcat gccaggctgc aagaccctca acttcacctt ggacctgtca    1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc    1500
ctgctcctga gccgcaacag catctcgcag gcagtcaacg gctcacaatt tatgccgctg    1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct    1620
ttcacggagc tgccgcggct ggaggccctg gacctcagct acaacagcca gcccttcagc    1680
atgcagggcg tgggtcacaa cctcagcttt gtggcacagc tgccggccct gcgctatctc    1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgctg    1800
cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat    1860
ctccacttct tccgaggcct gaggagcctg gtccggttgg atctgtccca gaatcgcctg    1920
cataccctct tgccacgcac cctggacaac ctccccaaga gcctgcggct gctgcgtctc    1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa    2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaatgga    2100
acccagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt    2160
tttgctctgg ccaccaggct gcgagagctc aacctcagtg ccaacgccct caagacggtg    2220
gagccctcct ggttcggttc tctagcgggc accctgaaag tcctagatgt gactggcaac    2280
cccctgcact gcgcctgtgg gcggccttc gtggacttct tgctggaggt gcaggctgca    2340
gtgcccggcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc    2400
atctttgcgc aggatctgcg cctctgcctg gatgaggccc tctcctggga ctgttttggc    2460
```

<210> 29
<211> 1032
<212> PRT
<213> Mus musculus

<400> 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
370 375 380

Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr
420 425 430

Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
435 440 445

Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
450 455 460

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
1025 1030

<210> 30
<211> 821
<212> PRT
<213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
370 375 380

Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr
420 425 430

Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
435 440 445

Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
450 455 460

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly
820

<210> 31
<211> 3200
<212> DNA
<213> Mus musculus

<400> 31
tgtcagaggg agcctcggga gaatcctcca tctcccaaca tggttctccg tcgaaggact 60

ctgcacccct tgtccctcct ggtacaggct gcagtgctgg ctgagactct ggccctgggt 120

accctgcctg ccttcctacc ctgtgagctg aagcctcatg gcctggtgga ctgcaattgg 180

ctgttcctga agtctgtacc ccgtttctct gcggcagcat cctgctccaa catcacccgc 240

ctctccttga tctccaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc 300

aacctgcggc agctgaacct caagtggaac tgtccaccca ctggccttag cccccctgcac 360

ttctcttgcc acatgaccat tgagcccaga accttcctgg ctatgcgtac actggaggag 420

ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctggtgaat 480

ctgagcctga gccacaccaa catcctggtt ctagatgcta acagcctcgc cggcctatac 540

agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccccctg cacaggagcg 600

gtgaaggtga ccccaggcgc cctcctgggc ctgagcaatc tcacccatct gtctctgaag 660

tataacaacc tcacaaaggt gccccgccaa ctgcccccca gcctggagta cctcctggtg 720

tcctataacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttcga 780

gtacttgatg tgggtgggaa ttgccgtcgc tgcgaccatg cccccaatcc ctgtatagaa 840

tgtggccaaa agtccctcca cctgcaccct gagaccttcc atcacctgag ccatctggaa 900

ggcctggtgc tgaaggacag ctctctccat acactgaact cttcctggtt ccaaggtctg 960

gtcaacctct cggtgctgga cctaagcgag aactttctct atgaaagcat caaccacacc 1020

aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag 1080

aaggtatcct ttgcccgcct ccacctggca agttccttca agaacctggt gtcactgcag 1140

gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg 1200

gccgatctgc ccaaactcca cactctgcat cttcaaatga acttcatcaa ccaggcacag 1260

ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcatc 1320

agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag 1380

gagctgttgt ctgcggatcc tcacccagct ccactgagca cccctgcttc taagaacttc 1440

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact 1500
atcaagccag agatgtttgt caatctctca cgcctccagt gtcttagcct gagccacaac 1560
tccattgcac aggctgtcaa tggctctcag ttcctgccgc tgactaatct gcaggtgctg 1620
gacctgtccc ataacaaact ggacttgtac cactggaaat cgttcagtga gctaccacag 1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac 1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttagcctggc acacaatgac 1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc 1860
ggcaacggta tgggccgcat gtgggatgag gggggccttt atctccattt cttccaaggc 1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcatatcct ccggccccag 1980
aaccttgaca acctccccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct 2040
ttctttaact ggaccagtct gtccttcctg cccaacctgg aagtcctaga cctggcaggc 2100
aaccagctaa aggccctgac caatggcacc ctgcctaatg gcaccctcct ccagaaactg 2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag 2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg 2280
cccattgtga tgaacctgac agttctagac gtgagaagca accctctgca ctgtgcctgt 2340
ggggcagcct tcgtagactt actgttggag gtgcagacca aggtgcctgg cctggctaat 2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg 2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcact cttggctgtg 2520
gccgtgggca tggtggtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt 2580
tttcatctgt gcctggcatg gctacctttg ctggcccgca gccgacgcag cgcccaagct 2640
ctcccctatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg 2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt 2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc 2820
tatgggagcc gcaagactct atttgtgctg gcccacacgg accgcgtcag tggcctcctg 2880
cgcaccagct tcctgctggc tcagcagcgc ctgttggaag accgcaagga cgtggtggtg 2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgctatg tgcgactgcg ccagcgtctc 3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggcc 3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgccgg 3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcatctt catgcctggt 3180
tcccgagttg ctctgcctgc 3200

<210> 32
<211> 2463
<212> DNA
<213> Mus musculus

<400> 32
atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtacaggc tgcagtgctg 60

gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120

ggcctggtgg actgcaattg gctgttcctg aagtctgtac cccgtttctc tgcggcagca 180

tcctgctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240

tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300

actggcctta gcccccctgca cttctcttgc cacatgacca ttgagcccag aaccttcctg 360

gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420

ctgcccagct ccctggtgaa tctgagcctg agccacacca acatcctggt tctagatgct 480

aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540

aagaacccct gcacaggagc ggtgaaggtg accccaggcg ccctcctggg cctgagcaat 600

ctcacccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660

agcctggagt acctcctggt gtcctataac ctcattgtca agctggggcc tgaagacctg 720

gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780

gccccccaatc cctgtataga atgtggccaa aagtccctcc acctgcaccc tgagaccttc 840

catcacctga gccatctgga aggcctggtg ctgaaggaca gctctctcca tacactgaac 900

tcttcctggt tccaaggtct ggtcaacctc tcggtgctgg acctaagcga gaactttctc 960

tatgaaagca tcaaccacac caatgccttt cagaacctaa cccgcctgcg caagctcaac 1020

ctgtccttca attaccgcaa gaaggtatcc tttgcccgcc tccacctggc aagttccttc 1080

aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctcgctcaac 1140

aagtacacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaatg 1200

aacttcatca accaggcaca gctcagcatc tttggtacct tccgagccct tcgctttgtg 1260

gacttgtcag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320

gcagatgatg cagagcagga ggagctgttg tctgcggatc ctcacccagc tccactgagc 1380

acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440

tctcggaaca acctggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500

tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgccg 1560

ctgactaatc tgcaggtgct ggacctgtcc cataacaaac tggacttgta ccactggaaa 1620

tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680

agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740

cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800

gtgaggtttc ttgacttcag cggcaacggt atgggccgca tgtgggatga ggggggcctt 1860

tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920

ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980

ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttcct gcccaacctg 2040

gaagtcctag acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaat 2100

ggcaccctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160

ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220

gtggatcgct cctggtttgg gcccattgtg atgaacctga cagttctaga cgtgagaagc 2280

aaccctctgc actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340

aaggtgcctg gcctggctaa tggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400

agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460

ggc 2463

<210> 33
<211> 1032
<212> PRT
<213> Homo sapiens

<400> 33

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu
420 425 430

Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu
435 440 445

Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu
515 520 525

Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu
1025 1030

<210> 34
<211> 820
<212> PRT
<213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420 425 430

Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu
435 440 445

Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu
515 520 525

Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Ala
820

<210> 35
<211> 3352
<212> DNA
<213> Homo sapiens

<400> 35
aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60

ggacctcgag tgtgaagcat ccttccctgt agctgctgtc cagtctgccc gccagaccct 120

ctggagaagc ccctgccccc cagcatgggt ttctgccgca gcgccctgca cccgctgtct 180

ctcctggtgc aggccatcat gctggccatg accctggccc tgggtacctt gcctgccttc 240

ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcaccccgt ggcaatgtca ccagcctttc cttgtcctcc 360
aaccgcatcc accacctcca tgattctgac tttgcccacc tgcccagcct gcggcatctc 420
aacctcaagt ggaactgccc gccggttggc ctcagcccca tgcacttccc ctgccacatg 480
accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac 540
aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat 600
accaacatcc tgatgctaga ctctgccagc ctcgccggcc tgcatgccct gcgcttccta 660
ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccg 720
ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact 780
gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgtccta caaccgcatc 840
gtcaaactgg cgcctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc 900
ggaaattgcc gccgctgcga ccacgctccc aacccctgca tggagtgccc tcgtcacttc 960
ccccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag 1020
gacagttctc tctcctggct gaatgccagt tggttccgtg ggctgggaaa cctccgagtg 1080
ctggacctga gtgagaactt cctctacaaa tgcatcacta aaaccaaggc cttccagggc 1140
ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggt gtcctttgcc 1200
cacctgtctc tggccccttc cttcgggagc ctggtcgccc tgaaggagct ggacatgcac 1260
ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccg cctgcccatg 1320
ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg 1380
gccttccctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag 1440
ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac 1500
cttgctccgg ccccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc 1560
ctcaacttca ccttggatct gtcacggaac aacctggtga ccgtgcagcc ggagatgttt 1620
gcccagctct cgcacctgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc 1680
aatggctccc agttcctgcc gctgaccggt ctgcaggtgc tagacctgtc ccgcaataag 1740
ctggacctct accacgagca ctcattcacg gagctaccgc gactggaggc cctggacctc 1800
agctacaaca gccagccctt tggcatgcag ggcgtgggcc acaacttcag cttcgtggct 1860
cacctgcgca ccctgcgcca cctcagcctg gcccacaaca acatccacag ccaagtgtcc 1920
cagcagctct gcagtacgtc gctgcgggcc ctggacttca gcggcaatgc actgggccat 1980
atgtgggccg agggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg 2040

```
ctggacttgt cccagaaccg cctgcacacc ctcctgcccc aaaccctgcg caacctcccc   2100

aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc   2160

ctccacttcc tgcccaaact ggaagtcctc gacctggcag gaaaccggct gaaggccctg   2220

accaatggca gcctgcctgc tggcacccgg ctccggaggc tggatgtcag ctgcaacagc   2280

atcagcttcg tggcccccgg cttcttttcc aaggccaagg agctgcgaga gctcaacctt   2340

agcgccaacg ccctcaagac agtggaccac tcctggtttg ggcccctggc gagtgccctg   2400

caaatactag atgtaagcgc caaccctctg cactgcgcct gtggggcggc ctttatggac   2460

ttcctgctgg aggtgcaggc tgccgtgccc ggtctgccca gccgggtgaa gtgtggcagt   2520

ccgggccagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag   2580

gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg   2640

cccatgctgc atcacctctg tggctgggac ctctggtact gcttccacct gtgcctggcc   2700

tggcttccct ggcgggggcg gcaaagtggg cgagatgagg atgccctgcc ctacgatgcc   2760

ttcgtggtct tcgacaaaac gcagagcgca gtggcagact gggtgtacaa cgagcttcgg   2820

gggcagctgg aggagtgccg tgggcgctgg gcactccgcc tgtgcctgga ggaacgcgac   2880

tggctgcctg gcaaaaccct ctttgagaac ctgtgggcct cggtctatgg cagccgcaag   2940

acgctgtttg tgctggccca cacggaccgg gtcagtggtc tcttgcgcgc cagcttcctg   3000

ctggcccagc agcgcctgct ggaggaccgc aaggacgtcg tggtgctggt gatcctgagc   3060

cctgacggcc gccgctcccg ctacgtgcgg ctgcgccagc gcctctgccg ccagagtgtc   3120

ctcctctggc cccaccagcc cagtggtcag cgcagcttct gggcccagct gggcatggcc   3180

ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa   3240

tagccgtgag ccggaatcct gcacggtgcc acctccacac tcacctcacc tctgcctgcc   3300

tggtctgacc ctcccctgct cgcctccctc accccacacc tgacacagag ca           3352
```

```
<210>  36
<211>  2460
<212>  DNA
<213>  Homo sapiens

<400>  36
atgggtttct gccgcagcgc cctgcacccg ctgtctctcc tggtgcaggc catcatgctg     60

gccatgaccc tggccctggg taccttgcct gccttcctac cctgtgagct ccagccccac    120

ggcctggtga actgcaactg gctgttcctg aagtctgtgc cccacttctc catggcagca    180

ccccgtggca atgtcaccag cctttccttg tcctccaacc gcatccacca cctccatgat    240
```

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgccg 300

gttggcctca gccccatgca cttcccctgc cacatgacca tcgagcccag caccttcttg 360

gctgtgccca ccctggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg 420

ctgcccaaat ccctcatatc cctgtccctc agccatacca acatcctgat gctagactct 480

gccagcctcg ccggcctgca tgccctgcgc ttcctattca tggacggcaa ctgttattac 540

aagaacccct gcaggcaggc actggaggtg gccccgggtg ccctccttgg cctgggcaac 600

ctcacccacc tgtcactcaa gtacaacaac ctcactgtgg tgccccgcaa cctgccttcc 660

agcctggagt atctgctgtt gtcctacaac cgcatcgtca aactggcgcc tgaggacctg 720

gccaatctga ccgccctgcg tgtgctcgat gtgggcggaa attgccgccg ctgcgaccac 780

gctcccaacc cctgcatgga gtgccctcgt cacttccccc agctacatcc cgataccttc 840

agccacctga gccgtcttga aggcctggtg ttgaaggaca gttctctctc ctggctgaat 900

gccagttggt tccgtgggct gggaaacctc cgagtgctgg acctgagtga gaacttcctc 960

tacaaatgca tcactaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac 1020

ctgtccttca attaccaaaa gagggtgtcc tttgcccacc tgtctctggc cccttccttc 1080

gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttccg ctcactcgat 1140

gagaccacgc tccggccact ggcccgcctg cccatgctcc agactctgcg tctgcagatg 1200

aacttcatca accaggccca gctcggcatc ttcagggcct tccctggcct gcgctacgtg 1260

gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca 1320

gatggagggg agaaggtctg gctgcagcct ggggaccttg ctccggcccc agtggacact 1380

cccagctctg aagacttcag gcccaactgc agcaccctca acttcacctt ggatctgtca 1440

cggaacaacc tggtgaccgt gcagccggag atgtttgccc agctctcgca cctgcagtgc 1500

ctgcgcctga gccacaactg catctcgcag gcagtcaatg gctcccagtt cctgccgctg 1560

accggtctgc aggtgctaga cctgtcccgc aataagctgg acctctacca cgagcactca 1620

ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc 1680

atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgcaccct gcgccacctc 1740

agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgctg 1800

cgggccctgg acttcagcgg caatgcactg ggccatatgt gggccgaggg agacctctat 1860

ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgtccca gaaccgcctg 1920

cacaccctcc tgccccaaac cctgcgcaac ctccccaaga gcctacaggt gctgcgtctc 1980

cgtgacaatt acctggcctt ctttaagtgg tggagcctcc acttcctgcc caaactggaa 2040

gtcctcgacc tggcaggaaa ccggctgaag gccctgacca atggcagcct gcctgctggc 2100

acccggctcc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc ccccggcttc 2160

ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220

gaccactcct ggtttgggcc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280

cctctgcact gcgcctgtgg ggcggccttt atggacttcc tgctggaggt gcaggctgcc 2340

gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccgg gccagctcca gggcctcagc 2400

atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 37
accttgcctg ccttcctacc ctgtga 26

<210> 38
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 38
gtccgtgtgg gccagcacaa a 21

<210> 39
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 39
tccatgacgt ttttgatgtt 20

<210> 40
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 40
tccataacgt ttttgatgtt 20

<210> 41
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 41
tccatcacgt ttttgatgtt 20

<210> 42
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 42
tccattacgt ttttgatgtt 20

<210> 43
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 43
tccatggcgt ttttgatgtt 20

<210> 44
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 44
tccatgccgt ttttgatgtt 20

<210> 45
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45
tccatgtcgt ttttgatgtt 20

<210> 46
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 46
tccatgatgt ttttgatgtt 20

<210> 47
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 47
tccatgaagt ttttgatgtt 20

<210> 48
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 48
tccatgaggt ttttgatgtt 20

<210> 49
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 49
tccatgacat ttttgatgtt 20

<210> 50
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
tccatgacct ttttgatgtt 20

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 51
tccatgactt ttttgatgtt 20

<210> 52
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 52
tccatgacgc ttttgatgtt 20

<210> 53
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 53
tccatgacga ttttgatgtt 20

<210> 54
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 54
tccatgacgg ttttgatgtt 20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 55
tccatgacgt ctttgatgtt 20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 56
tccatgacgt atttgatgtt 20

<210> 57
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 57
tccatgacgt gtttgatgtt 20

<210> 58
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 58
tcgtcgtttt gtcgttttgt cgtt 24

<210> 59
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 59
tgctgctttt gtgcttttgt gctt 24

<210> 60
<211> 20
<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 60
tccatgacgt tcctgatgct 20

<210> 61
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 61
tccatgagct tcctgatgct 20

<210> 62
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus oligopeptide

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (7)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(15)
<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1 5 10 15

<210> 63
<211> 16
<212> PRT
<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys
1 5 10 15

<210> 64
<211> 16
<212> PRT
<213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys
1 5 10 15

<210> 65
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus oligopeptide

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr
            20   25   30

<210> 66
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
            20   25   30

<210> 67
<211> 31
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 68
<211> 31
<212> PRT
<213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His
1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr
20 25 30

<210> 69
<211> 31
<212> PRT
<213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

1 5 10 15

Ser Phe Ser Glu Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr
20 25 30

<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 70
tccaggactt ctctcaggtt 20